# DESCRIPTION

# COMPOSITIONS AND METHODS RELATED TO FLAVIVIRUS ENVELOPE PROTEIN DOMAIN III ANTIGENS

## BACKGROUND OF THE INVENTION

This application claims priority to U.S. Provisional Patent Applications serial numbers 60/403,893 filed on August 16, 2002 and 60/445,581 filed February 6, 2003, each of which is incorporated in its entirety herein by reference.

The government may own rights in the present invention pursuant to contract number U90/CCU618754-01 from U.S. Department of Health and Human Services Centers for Disease Control.

### 1. Field of the Invention

The present invention relates generally to the fields of virology, immunology and diagnostics. More particularly, it concerns antibodies directed to and antigens derived from flavivirus envelope protein domain III in compositions and methods for detection of various members of the genus *flavivirus*.

### 2. Description of Related Art

West Nile virus (WN) is a member of the Japanese encephalitis (JE) serocomplex of the genus *Flavivirus* (Family *Flaviviridae*). This virus was first isolated from a febrile woman in the West Nile province of Uganda in 1937, and now has an almost worldwide distribution including parts of Africa, Asia, Europe and, most recently, North America. Kunjin virus, now re-classified as a subtype of West Nile virus, is found in Australasia.

Since 1999, the United States has experienced annual epidemics of WN disease in humans and animals over an expanding geographical range. WN virus has been isolated in 44 states, and more than 4,100 cases of human disease resulting in 284 deaths had been reported during 2002 (MMWR , 2002a). Several of these cases are suspected to have originated from virus transmitted during blood transfusion and/or organ transplantation (MMWR, 2002b). Outbreaks of WN disease with neurological manifestations have also been reported in Eastern Europe, North Africa and Israel since the mid-1990s (reviewed by Murgue *et al.*, 2002).

Other members of the JE serocomplex include JE virus, found throughout Asia, St. Louis encephalitis (SLE) virus, found in the Americas, and Murray Valley encephalitis (MVE) virus, found in Australia and New Guinea. These viruses are antigenically similar to WN virus, and their co-circulation in several regions of the world has complicated the specific diagnosis of infections by these viruses in humans and other hosts (Fonseca *et al.*, 1991; Martin *et al.*, 2002). Current protocols for the serological diagnosis of WN virus infection in the United States rely primarily on preliminary screening for WN virus-reactive IgM/IgG antibody by capture ELISA and confirmation by plaque reduction neutralization test (PRNT) (CDC, 2001), a process which results in considerable delays in the reliable reporting of accurate case numbers, and requires the confirmatory testing to be performed in specialized laboratories.

Current diagnostic assays utilize either ELISA or dipstick formats for identification of flavivirus infection (PanBio, Integrated Diagnostics (Dobler *et al.*, 1996, Niedrig *et al.*, 2001, Yoshii *et al.*, 2003)). A number of assays are available for the detection of dengue virus infection. These assays utilize antigen capture and antibody-based ELISAs and dipsticks for detection of virus specific IgG or IgM. Diagnosis of TBE infection depends on IgG-based ELISA assays that are available in Europe (Dobler *et al.*, 1996, Niedrig *et al.*, 2001, Yoshii *et al.*, 2003). However, these tests have limitations with both sensitivity and cross-reactivity with other flaviviruses (Niedrig *et al.*, 2001).

The recent utilization of subviral particles (SVP) in an ELISA-based diagnostic test for tick borne encephalitis TBE infection shows promise (Yoshii *et al.*, 2003). Since this assay uses intact viral M and E proteins it is likely that the pitfalls that affect the use of complete viral antigen (*e.g.*, cross-reactivity) may impede the employment of this assay in diagnostic settings.

The use of RT-PCR is also a potential method for diagnosis of flavivirus infection. However, RT-PCR assays have the significant limitation of requiring advanced techniques, equipment and reagents that require a cold-chain for stability. In addition, RT-PCR detects the presence of virus in patient serum, a condition that is not usually met when patients come to a hospital as the virus is frequently cleared from the bloodstream by the onset of symptoms. Clearly, there is a need to improve the current reagents used for diagnosis of West Nile and TBE virus infections.

## SUMMARY OF THE INVENTION

Embodiments of the invention include the use of recombinant envelope protein domain III (rDIII or rD3) derived from West Nile virus (WN), tick borne encephalitis serocomplex viruses (TBE), and/or other flaviviruses as a reagent(s) to detect the presence of anti-WN or anti-TBE antibodies in a subject, *e.g.*, naturally infected primates, including humans. Certian embodiments include polypeptides derived from WN rDIII that are sensitive and very specific for WN virus infection and can also differentiate between closely related mosquito-borne flaviviruses. Some embodiments of the invention include the use of poly-peptides derived form TBE rDIII (rD3) as a diagnostic antigen to the TBE serocomplex of flaviviruses. While differentiation between the very similar TBE viruses could not be achieved, some of the polypeptide reagents were highly specific for the tick-borne flaviviruses and were much more specific than mouse brain-derived viral antigen in differentiating flavivirus positive sera in the ELISA format.

The development of a specific and sensitive diagnostic assay for detection of *flavivirus* infection will greatly enhance the ability to identify, track, and treat diseases caused by these viruses. The present invention takes advantage of the observation that a flavivirus envelope protein domain III (DIII) antigen can be used to specifically detect serocomplexes of flavivirus and antibodies against certain serocomplexes or certain flaviviruses, *e.g.*, West Nile virus. In addition, the present invention takes advantage of the observation that certain West Nile virus envelope protein domain III (WN-DIII) antigens can be used to specifically detect West Nile virus and antibodies against West Nile virus. Various embodiments of the invention are directed to compositions and methods related to detecting West Nile virus or TBE serocomplex viruses or antibodies in a subject, patient, animal, biological or other type of sample.

The present invention includes compositions and methods for the detection or diagnosis of flavivirus, TBE viruses or West Nile virus. Recombinant West Nile virus envelope protein domain III (WN-rDIII) or a recombinant TBE serocomplex virus envelope protein domain III (TBE-rDIII) can be expressed in *E. coli* as a fusion protein to produce a soluble protein that can be purified. Rabbit antisera raised against WN-rDIII or TBE-rDIII shows virus or serocomplex specificity, respectively, in physical and biological assays. Removal of a non-viral fusion component typically improves the specificity and signal intensity for WN-rDIII or TBE-rDIII.

In certain embodiments of the invention, methods for screening for a flavivirus in a subject include a) contacting a sample from the subject with a composition comprising a flavivirus envelope protein domain III polypeptide under conditions that permit formation of

specific immunocomplex between any antibody in the sample and the envelope protein domain III polypeptide; and b) detecting whether a specific immunocomplex is formed. An envelope protein domain III polypeptide refers to a polypeptide including the amino acids that define domain III, a structural element of the flavivirus envelope protein, for example amino acid sequences 292 to 402 of SEQ ID NO:3, amino acid sequences set forth in SEQ ID NO:4-21 or homologous sequences from other flaviviruses. Homologous envelope protein domain III sequences from other flavivirus typically have an identity of at least 70, 75, 80, 85, 90, 95 percent or greater to the amino acid sequence 292-402 set forth in SEQ ID NO: 3 or the amino acid seqeunces set forth in SEQ ID NO:4-21. Additionally, a specific immunocomplex refers to a complex between a polypeptide containing an epitope recognized by an antibody and the antibody that recognizes the epitope where the complex can be detected and distinguish above any non-specific or background interactions. The envelope protein domain III polypeptide may be a dengue virus envelope protein domain III polypeptide, yellow fever virus envelope protein domain III polypeptide, West Nile virus envelope protein domain III polypeptide, St. Louis encephalitis virus envelope protein domain III polypeptide, Murray valley encephalitis virus envelope protein domain III polypeptide, a Central European encephalitis (CEE) virus envelope protein domain III polypeptide, a Russian spring-summer encephalitis (RSSE) virus envelope protein domain III polypeptide, a Langat (LGT) virus envelope protein domain III polypeptide, a Powassan virus (POW) envelope protein domain III polypeptide, an Alkhurma (ALK) envelope protein domain III polypeptide, a Kyasanur Forest disease (KFD) virus envelope protein domain III polypeptide, an Omsk hemorrhagic fever (OHF) virus envelope protein domain III polypeptide or a combination or variant thereof. In particular embodiments, the envelope protein domain III polypeptide is a West Nile virus enevelope protein domain III polypeptide or a variant thereof. In other embodiments, the envelope protein domain III polypeptide is derived from a CEE or a RSSE enevelope protein domain III polypeptide or a variant thereof. The envelope protein domain III polypeptide may include 5 , 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60. 65. 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, or 110 contiguous amino acids of a flavivirus envelope protein domain III polypeptide or a variant thereof. It is contemplated that 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more carboxy and/or amino terminal amino acids flanking the envelope protein domain III may also be included in an envelope protein domain III polypeptide. In certain embodiments, an amino acid sequence that is about or at least 50%, 55%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, or any value therebewteen, identical to amino aicd 292-402 of SEQ ID NO:3 and/or SEQ ID NO:8-21 is contemplated. A domain III polypeptide may include

the amino acids 292-402 as set forth in SEQ ID NO:3, the amino acids 1-111 as set forth in SEQ ID NO:21, the amino acids as set forth in SEQ ID NO:4-20, or variants thereof. Some embodiments of the invention further comprise at least a second envelope protein domain III polypeptide. A second envelope protein domain III polypeptide may be selected from SEQ ID NO:3-21 or a similar sequence from other flaviviruses or closely related viruses. The envelope protein domain III polypeptide may be prepared by isolating a recombinant or non-recombinant envelope protein domain III polypeptide. The envelope protein domain III polypeptide may be denatured or non-denatured. In particular embodiments the envelope protein domain III polypeptide is prepared by isolating a recombinant envelope protein domain III polypeptide fusion protein. In certain embodiments, a recombinant envelope protein domain III polypeptide may be cleaved by an appropriate protease to separate the envelope protein domain III polypeptide from its viral or non-viral fusion partner (*e.g.*, GST, his-tag or MBP). A envelope protein domain III polypeptide may be obtained from bacteria comprising an expression vector encoding the envelope protein domain III polypeptide or envelope protein domain III polypeptide fusion protein. The envelope protein domain III polypeptide or fusion protein may be obtained from a mammalian or insect cell comprising an expression vector encoding the envelope protein domain III polypeptide or fusion protein.

In certain embodiments it is contemplated an envelope protein domain III polypeptide may be used in conjunction with 1, 2, 3, 4, 5, 6, or more additional antigens derived the same or other members of the flavivirus genus family. These polypeptides may be used in a variety of formats including, but not limited to ELISA and peptide array formats.

In various embodiments, samples may be derived from a variety of subjects infected with or suspected to be infected with a flavivirus, including WN or a TBE serocomplex virus. The subjects include, but are not limited to an animal, a bird, a human, a mosquito, a tick or other host organism for a flavivirus.

The step of determining whether an immunocomplex is formed may be accomplished by a number of ways well known to those of ordinary skill in the art. The immunocomplex may be detected by ELISA, Western blotting, dipstick or peptide array. In other embodiments, an immunocomplex is detected using anti-antibody secondary reagents. Anti-antibody secondary reagents refer to agents that specifically bind or detect an antibody. Compounds of the invention may be labeled with a detecting agent, which may be colorimetric, enzymatic, radioactive, chromatographic or fluorescent. The antigen may be affixed to a solid non-reactive support, which refers to a compound that will not react with antigens of the invention or antibodies in any sample. The support may be a plate or assay dish, and be made of any non-reactive material,

including, glass, plastic, silicon or the like. An antibody may include, but is not limited to an IgA, an IgG or an IgM antibody.

Various embodiments include methods of identifying a flavivirus in a subject comprising a) contacting a sample from the subject with a composition comprising at least one flavivirus envelope protein domain III polypeptide under conditions that permit formation of specific immunocomplex between any antibody in the sample and the envelope protein domain III polypeptide; and b) detecting whether a specific immunocomplex is formed.

Certain embodiments of the invention include compositions for testing a sample for flavivirus or antibodies to flavivirus comprising an isolated flavivirus envelope protein domain III polypeptide. In particular embodiments, the flavivirus envelope protein domain III polypeptide is a West Nile virus or a TBE serocomplex virus envelope protein domain III polypeptide or variants thereof. A West Nile virus envelope protein domain III polypeptide may be derived from West Nile strains 382-99, EthAn4766, 385-99, Kunjin MRM16, Golblum, TL44, DakAnMg, 804994 or a variant thereof, which may be obtained through the World Arbovirus Reference Collection at the University of Texas Medical Branch at Galveston or similar depositories such as the American Type Culture Collection. A TBE serocomplex virus may include a Central European encephalitis (CEE) virus, a Russian spring-summer encephalitis (RSSE) virus, a Langat (LGT) virus, a Powassan virus (POW), an Alkhurma (ALK), a Kyasanur Forest disease (KFD) virus, or an Omsk hemorrhagic fever (OHF) virus, which may be obtained through the World Arbovirus Reference Collection at the University of Texas Medical Branch at Galveston or similar depositories such as the American Type Culture Collection. The composition may include a flavivirus envelope protein domain III polypeptide, which may comprise 10, 11, 12, 13, 14, 15, 16, 17, 18 , 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, or more, as well as values there between, of consecutive amino acids of the envelope protein domain III polypeptide or variants thereof. In particular embodiments, the composition may comprise the amino acid sequence as set forth in, or is about or at least 50%, 55%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, or any value therebewteen, identical to, one or more of SEQ ID NO:3–21. The envelope protein domain III polypeptide may be operatively linked to a substrate such as a plate, a microtiter plate, a bead, or a microarray.

Embodiments of the invention also include compositions for testing a sample for West Nile virus or a TBE serocomplex virus comprising an isolated flavivirus or flavivirus envelope protein domain III polypeptide as described above and incorporated here by reference.

Embodiments of the invention also include kits comprising any of the components of the invention described above, in a suitable container means. Kits may include one or more

flavivirus, TBE serocomplex virus or West Nile virus envelope protein domain III antigens. In still further embodiments, antigens are from the same or different strains. Such antigens may be in the same or in separate compositions. Kits may further include non-reactive supports in which antigens of the invention are affixed or attached. Kits may also include secondary antibody reagents and/or other detection reagents. Antigens or antibodies in the kits may be labeled. Labels may be colorimetric, enzymatic, radioactive, or fluorescent. The envelope protein domain III polypeptide may be a dengue fever virus envelope protein domain III polypeptide, yellow fever virus envelope protein domain III polypeptide, West Nile virus envelope protein domain III polypeptide, St. Louis encephalitis virus envelope protein domain III polypeptide, Murray Valley encephalitis virus envelope protein domain III polypeptide, a Central European encephalitis (CEE) virus envelope protein domain III polypeptide, a Russian spring-summer encephalitis (RSSE) virus envelope protein domain III polypeptide, a Langat (LGT) virus envelope protein domain III polypeptide, a Powassan virus (POW) envelope protein domain III polypeptide, an Alkhurma (ALK) envelope protein domain III polypeptide, a Kyasanur Forest disease (KFD) virus envelope protein domain III polypeptide, an Omsk hemorrhagic fever (OHF) virus envelope protein domain III polypeptide or a combination thereof. In particular embodiments, the envelope protein domain III polypeptide is a West Nile virus envelope protein domain III polypeptide. A kit may include compositions for screening for West Nile or TBE serocomplex virus antibodies in a subject comprising: a) an assay plate comprising a multiplicity of microtiter wells comprising a composition comprising at least one envelope protein domain III polypeptide capable of binding a flavivirus antibody in the sample that can specifically bind to at least one envelope protein domain III polypeptide; and b) a container means comprising a labeled secondary antibody having specific binding affinity for a flavivirus antibody in the sample that can specifically bind to at least one envelope protein domain III polypeptide.

Embodiments of the invention also include methods of screening for flavivirus in a subject comprising: a) contacting a sample from the subject with a composition from the kit under binding conditions; and, b) detecting whether a specific immunocomplex is formed between an antibody and the at least one envelope protein domain III polypeptide.

Various embodiments of the invention include vaccine compositions comprising a flavivirus, TBE serocomplex or West Nile envelope protein domain III polypeptide as described herein. The vaccine composition may further comprise an adjuvant(s) and an excipient(s) known in the art.

Other embodiments of the invention include an antibody or antibodies that selectively bind to an epitope in a envelope protein domain III of a flavivirus, TBE serocomplex or West

Nile virus envelope protein. The epitope may be present in a West Nile or a TBE serocomplex envelope protein domain III polypeptide or a variant thereof.

It is contemplated that any embodiment of a method or composition described herein can be implemented with respect to any other method or composition described herein.

The use of the word "a" or "an" when used in conjunction with the term "comprising" in the claims and/or the specification may mean "one," but it is also consistent with the meaning of "one or more," "at least one," and "one or more than one."

The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternative are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and "and/or."

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

## BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

**FIG. 1** illustrates an exemplary amino acid alignment of envelope protein domain IIIs from various flaviviruses.

**FIG. 2** illustrates a two-dimensional schematic of the topology and structure of a flavivirus envelope protein.

**FIG. 3** illustrates the binding of rabbit antiserum raised against WN recombinant envelope protein domain III antigen to flavivirus envelope proteins in western blot assays with whole virus antigens of (1) WN, (2) JE, (3) SLE, and (4) MVE viruses.

**FIG. 4** illustrates Western blot analysis or WN envelope protein domain III specific monoclonal antibodies 5H10, 3A3, 7H2, 5C5, 3D9, and a polyclonal antiserum to WN envelope protein domain III.

**FIG. 5** illustrates the results of an exemplary PRNT assay showing the neutralization activity of rabbit anti-envelope protein domain III sera.

**FIG. 6** illustrates an envelope protein domain III amino acid sequence variations for ten West Nile virus strains, and representative JE (Genbank accession U21057), SLE (Genbank accession M16614) and MVE (Genbank accession M24220) viruses. Dots (.) indicate conservation with the West Nile virus strain 385-99 sequence. Residues associated with escape from neutralization by Mabs or anti-envelope protein domain III serum for WN virus strains are shaded.

**FIG. 7** illustrates the binding of selected anti-flavivirus mouse immune ascitic fluids in an indirect ELISA protocol utilizing whole-virus JE serocomplex antigens (WN, JE, SLE, or MVE viruses) or recombinant WN envelope protein domain III. Error bars 1 standard deviation from the mean.

**FIG. 8** illustrates the binding of selected anti-flavivirus mouse immune ascitic fluids in an indirect ELISA protocol utilizing whole-virus JE serocomplex antigens (WN, JE, SLE, or MVE viruses) or recombinant WN envelope protein domain III cleaved from a GST fusion protein.

**FIG. 9A-9C** illustrates the binding of selected anti-flavivirus mouse immune ascitic fluids in an indirect ELISA protocol utilizing WN rDIII cleaved from an maltose binding protein (MBP) fusion protein, MBP WN rDIII fusion protein at 35 ng/well, and MBP WN rDIII fusion protein at 17.5 ng/well.

**FIG. 10** Phylogentic analysis of the flavivirus envelope protein domain III amino acid sequence. Analysis was performed using maximum parsimony analysis. The tree was rooted using the non-vector borne Rio Bravo virus.

**FIG. 11** Western blot of recombinant DIII. Ten ng of purified recombinant DIII was run on 12% SDS-PAGE gels and transferred to nitrocellulose. Blots were probed with homologous or heterologous anti-DIII serum. Asibi, yellow fever type strain; 17D, yellow fever vaccine strain; WN, West Nile virus; KFD, Kyasanur Forrest disease virus; KUM, central European TBE strain Kumlinge; LGT, Langat; OHF, Omsk hemorrhagic disease virus; POW, Powassan virus.

**FIG. 12A-12F** ELISAs using MIAF to detect virus derived antigen. Mouse brain virus-derived antigen was coated into 96 well plates at 1 HA unit per well and MIAF were tested in two-fold serial dilutions. Each value represents the mean of duplicate wells. The legend in panel B is for all six panels. The tick-borne flaviviruses are represented by open symbols.

**FIG. 13A-13F** ELISAs using virus derived antigen to detect IgG in rabbit anti-DIII specific antiserum. Antigens were coated in the plates as 1 HA unit per well and anti-DIII specific sera were tested in two-fold serial dilutions. Each value is the mean of duplicate wells.

The legend refers to rabbit anti-DIII specific sera and the legend in panel A is for all panels. Tick-borne flaviviruses are represented by open symbols. Note scale differences in the Y-axis.

**FIG. 14A-14H** ELISAs using rDIII to detect IgG in rabbit anti-DIII specific antiserum. Recombinant rDIII was coated into plates at 20 ng per well and DIII specific sera were tested in two-fold serial dilutions. Each value is the mean of duplicate wells. The legend for all panels refers to DIII specific sera and is presented in panel H. Tick-borne flaviviruses are represented by open symbols. Note scale differences in Y-axis.

**FIG. 15A-15H** ELISAs using rDIII to detect virus specific IgG in MIAF. Recombinant DIII was coated into plates at 20 ng per well and MIAF were tested in two-fold serial dilutions. Each value represents the mean of duplicate wells. The legend for all panels refers to MIAF and is presented in panel A. Tick-borne flaviviruses are represented by open symbols. Note scale differences in the Y-axis.

**FIG. 16** illustrates an exemplary amino acid alignment of envelope protein domain IIIs from various flaviviruses.

## DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

Various embodiments of the invention include compositions and methods related to flavivirus, TBE serocomplex flaviviruses (viruses) (TBE) or West Nile virus (WN) envelope protein domain III (DIII or D3) or recombinant DIII (rDIII or rD3) as an antigen for specific diagnosis or detection of flavivirus, TBE serocomplex viruses and/or WN virus. The flavivirus envelope protein (E) is the major virion surface protein. It plays an important role in virus attachment and entry into host cells, and is also an important target for virus neutralizing antibodies (Sanchez and Ruiz, 1996; Mandl *et al.*, 2000; Crill and Roehrig, 2001 ). The inventors describe the identification of residues associated with the neutralization of lineage I WN virus strain 385-99 (isolated in New York City in 1999) by monoclonal antibodies (MAbs) that bound to DIII, the putative receptor-binding domain, of the envelope protein.

Using these DIII-reactive MAbs and a polyclonal serum generated against a recombinant, bacterially-expressed WN virus rDIII fragment, the antigenic relationships between WN virus strains representative of genetic lineages I and II have been investigated and envelope protein domain III residues that constitute subtype specific epitopes have been indentified.

The present invention includes compositions and methods for the detection or diagnosis of a flavivirus, including compositions and methods for distinguishing between different flaviviruses or groups of flaviviruses. In particular embodiments, the flavivirus being detected is

the West Nile virus or a TBE serocomplex virus. Recombinant flavivirus, TBE virus or West Nile virus envelope protein domain III (rDIII) can be expressed in *E. coli* as a fusion protein to produce a soluble protein that can easily be purified. Rabbit antisera raised against a rDIII (rDIII) shows virus specificity in physical and biological assays. Removal of the fusion component improves specificity and signal intensity for a particular rDIII.

The serological diagnosis of infection by flaviviruses can be complicated by the presence of flavivirus cross-reactive antibodies that produce false-positive results for flavivirus infections, especially in regions where more than one virus is endemic. Current diagnostic reagents for tick-borne flavivirus infection have been found to cross-react with yellow fever or dengue positive sera. In certain embodiments, recombinant flavivirus envelope protein domain III (rDIII or rD3) can be used as a diagnostic reagent to differentiate between infection by mosquito- and tick-borne flaviviruses. Embodiments of the invention also include the use of rDIII in an ELISA-based format for differentiation between serum specific for either mosquito- or tick-borne flaviviruses, which may or may not differentiate among the members of the tick-borne encephalitis (TBE) serocomplex of flaviviruses. Sera derived against several TBE serocomplex rDIII were found to cross-react with heterologous rDIII within the TBE serocomplex, but not with those from mosquito-borne flaviviruses, in both Western blots and ELISAs. Mouse hyperimmune serum generated against TBE serocomplex viruses was also found to react specifically with TBE serocomplex rDIII, but not with rDIII from mosquito-borne viruses and vice versa. A similar test using virus-derived antigen was performed and a loss of both specificity and sensitivity was observed. These results indicate that flavivirus rDIII would be a useful reagent for the detection of infection by TBE serocomplex flaviviruses, several of which are potential biothreat agents, but may not provide the ability to differentiate between infections by separate members of the serocomplex.

## I. FLAVIVIRUS

West Nile virus and TBE viruses are members of the genus *Flavivirus*. The genus *Flavivirus* is a genera of the *Flaviviridae* family and includes the viral groups of Yellow Fever virus group, Tick-borne encephalitis virus group, Rio Bravo Group, Japanese encephalitis Group, Tyuleniy Group, Ntaya Group, Uganda S Group, Dengue Group, and Modoc Group. Members of the *Flavivirus* genus may produce a wide variety of disease states, such as fever, arthralgia, rash, hemorrhagic fever, and/or encephalitis. The outcome of infection is influenced by both the virus and host-specific factors, such as age, sex, genetic susceptibility, and/or pre-exposure to the same or a related agent. Some of the various diseases associated with members of the genus

*Flavivirus* are yellow fever; dengue fever; and West Nile, Japanese, and St. Louis encephalitis. For a review of Flaviviruses see Burke and Monath (2001), which is incorporated herein by reference.

Virions of the *Flaviviridae* generally contain one molecule of a linear positive-sense single stranded RNA genome of approximately 10,000-11,000 nucleotides that replicates in the cytoplasm of an infected cell. Typically the 5' end of the genome has a cap and the 3' end that may or may not have a poly (A) tract. Many members of the genus *Flavivirus* are transmitted by a vector such as an insect, in many cases the insect is a mosquito.

The viral genome of the *Flavivirus* genus is translated as a single polyprotein and is subsequently cleaved into mature proteins. The proteins encoded by the virus typically consist of structural and non-structural proteins. Generally, there are three structural proteins that typically include the envelope protein (E protein)(amino acids 275-787 of GenBank accession number NP_041724, incorporated herein by reference and SEQ ID NO:2), the core or capsid protein (C)(amino acids 1-92 of GenBank accession number NP_04-1724), and the pre-membrane protein (preM)(amino acids 105-223 of GenBank accession number NP_041724)(Yamshchikov *et al.*, 2001, incorporated herein by reference). The envelope protein is approximately 496 amino acids with an approximate molecular weight of 50 kDa and is often glycosylated. The envelope protein typically contains twelve conserved cysteine residues which form six disulfide bridges. The core protein is approximately 13 kDa and is rich in arginine and lysine residues. The pre-membrane protein is approximately 10 kDa and is cleaved during or after release of the virus from infected cells. A cleavage product of the prM protein remains associated with the virion and is approximately 8 kDa and is termed the membrane protein (M). Typically, it is the carboxy terminus of prM that remains associated with the virus particle as the M protein.

The flavivirus E protein is a dimer positioned parallel to virus surface. The ectodomain includes three domains I- Central domain (EI), II- Dimerization domain (EII), III- Immunogenic/Receptor binding domain (DIII) (FIG. 2). The amino acid sequence of an exemplary West Nile virus E protein Envelope protein domain III is set forth in SEQ ID NO:3. An amino acid alignment of various flavivirus DIIIs is presented in FIG. 1. The E protein envelope protein domain III is approximately 10.5 kDa with a single disulfide bridge. The E protein envelope protein domain III has an Ig-like fold, which is a β-barrel "type" configuration with no α-helices. Some flavivirus E protein domain IIIs contain a RGD integrin-binding motif.

Serological comparisons of West Nile virus strains have distinguished four major antigenic subtypes: a group of strains from Africa; strains from Europe and some Asian strains; strains from India; and strains of Kunjin virus from Australasia (Doherty *et al.*, 1968; Hammam *et al.*, 1966; Blackburn *et al.*, 1987; Calisher *et al.*, 1989; Morvan *et al.*, 1990). Subsequently, analyses of nucleotide sequences identified two major genetic lineages, designated I and II, which included some subtypes and which correlated well with the antigenic groupings. Genetic lineage I included European and some African strains, Kunjin virus strains, and Indian strains; lineage II comprised only African strains (Lanciotti *et al.*, 1999; Jia *et al.*, 1999; Scherret *et al.*, 2001).

The TBE virus group that is associated with human disease is distinct genetically and antigenically from the mosquito-borne viruses and are hence referred to as the TBE serocomplex. In addition to viruses that cause TBE, there are several other viruses within this serocomplex. Among these are the Langat (LGT) virus that is not known to infect humans in a natural environment, louping ill (LI) virus that causes encephaltitic disease normally in sheep, Powassan virus (POW) that also causes encephalitis, and the hemorrhagic fever associated viruses Alkhurma (ALK), Kyasanur Forest disease (KFD) and Omsk hemorrhagic fever (OHF) (Burke and Monath, 2001). Tick-borne encephalitis (TBE) is a disease endemic to vast areas from western Europe across Asia and into Japan and China. This disease is characterized by rapid onset of fever with subsequent development of potentially fatal encephalitis (Gritsun *et al.*, 2003). TBE found in Europe is typically less severe than that found in central and eastern Asia and the viruses that cause the different forms of the disease can be distinguished genetically and also by their tick vectors. Three subtypes of TBE have been described based on both serology and genetic data: central European encephalitis (CEE) (or western subtype), Siberian subtype TBE and Far-eastern subtype TBE (Heinz *et al.*, 2000). The disease caused by the latter two subtypes are often commonly referred to as Russian spring-summer encephalitis (RSSE). In addition, OHF, KFD and RSSE viruses are listed as potential biothreat agents by the National Institutes for Health and Centers for Disease Control. The possible introduction of these viruses by natural or artificial means into non-endemic areas, as well as the present extensive endemic regions, make the diagnosis of infection by these viruses a major public health objective. The lack of simple and accurate diagnostic assays makes the development of a TBE serocomplex diagnostic kit very important to rapid recognition of the causative agent of disease.

Various members of the *Flaviviridae* family are available through the American Type Culture Collection (Manassas Va.) under the following ATCC numbers: Dengue type 1 (VR-71), Ilheus (VR-73), Japanese encephalitis (VR-74), Murray Valley encephalitis (VR-77), Ntaya

(VR-78), St. Louis encephalitis (VR-80), Uganda S (VR-81), West Nile (VR-82), Zika (VR-84), Dengue type 4 (VR-217), Dengue type 2 (VR-222), Japanese encephalitis (VR-343), Dengue type 1 (VR-344), Dengue type 2 (VR-345), Edge hill (VR-377), Entebbe bat (VR-378), Kokobera (VR-379), Stratford (VR-380), Tembusu (VR-381), Dakar bat (VR-382), Ntaya (VR-78), Banzi (VR-414), Modoc (VR-415), Rio Bravo virus (VR-416), Cowbone ridge (VR-417), Bukalasa (VR-418), Montana myotis leukoencephalitis (VR-537), Bussuquara (VR-557), Sepik (VR-906), Cowbone ridge (VR-1253), Dengue type 2 (VR-1255), Dengue type 3 (VR-1256), Dengue type 4 (VR-1257), Ilheus (VR-1258), Rio Bravo virus (VR-1263), St. Louis encephalitis (VR-1265), West Nile (VR-1267), Dengue type 4 (VR-1490), West Nile (VR-1507), and West Nile (VR-1510), each of which is incorporated herein by reference.

## II. PROTEINACEOUS COMPOSITIONS

In various embodiments of the invention *Flavivirus*, TBE virus or West Nile virus polypeptides or proteins may be comprised in various proteinaceous compositions. These proteinaceous composition may be used in the detection of *flavivirus* members, vaccination against *flavivirus* members, as well as other methods and compositions described herein.

### A. Proteinaceous Compositions

In certain embodiments, the present invention concerns novel compositions comprising at least one proteinaceous molecule, such as a rDIII polypeptide (antigen) alone or in combination with other flavivirus envelope proteins, envelope protein domain IIIs or fragments thereof. As used herein, a "proteinaceous molecule," "proteinaceous composition," "proteinaceous compound," "proteinaceous chain" or "proteinaceous material" generally refers, but is not limited to, a protein of greater than about 200 amino acids or the full length endogenous sequence translated from a gene; a polypeptide of greater than about 100 amino acids; and/or a peptide of from about 3 to about 100 amino acids. All the "proteinaceous" terms described above may be used interchangeably herein. The term "antigen" refers to any substance or material that is specifically recognized by an antibody or T cell receptor. The term "epitope" refers to a specific antigenic determinant that is recognized by an antibody or T cell receptor. Thus, it is contemplated that the antigens of the invention may be truncations or only portions of a full-length polypeptide. For example, a "rDIII antigen" refers to a peptide or polypeptide containing contiguous amino acids of envelope protein domain III, including at least one envelope protein domain III epitope, but it may be fewer than a full-length amino acid sequence. Thus, an envelope protein domain III antigen may include a region of contiguous amino acids derived from any of SEQ ID NO:3-21.

SEQ ID NO:2 corresponds to protein accession number NP_041724, which is the sequence for a West Nile virus. SEQ ID NO:3 corresponds to amino acids 291-787 of SEQ ID NO:2 , which is a full-length processed E protein envelope protein domain III polypeptide sequence. Immunogenic regions of flavivirus envelope proteins have been described, and the present invention includes antigens that include one or more such regions.

In certain embodiments, a proteinaceous molecule comprising a TBE serocomplex virus or a West Nile virus envelope protein domain III antigen may comprise, be at least, or be at most 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 140, 150, 160, 170, 180, 190, 200 or greater contiguous amino acid residues, and any range derivable therein of SEQ ID NO:2, or SEQ ID NO:3-21.

As used herein, an "amino molecule" refers to any amino acid, amino acid derivative or amino acid mimic as would be known to one of ordinary skill in the art. In certain embodiments, the residues of the proteinaceous molecule are sequential, without any non-amino molecule interrupting the sequence of amino molecule residues. In other embodiments, the sequence may comprise one or more non-amino molecule moieties. In particular embodiments, the sequence of residues of the proteinaceous molecule may be interrupted by one or more non-amino molecule moieties.

Encompassed by certain embodiments of the present invention are peptides, such as, for example, a peptide comprising all or part of a flavivirus envelope antigen (including at least one epitope) of any subtype or clade. Peptides of the invention may comprise, be at least, or be at most 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111 contiguous amino acids, including all or part of any of SEQ ID NO:2-21.

Accordingly, the term "proteinaceous composition" encompasses amino molecule sequences comprising at least one of the 20 common amino acids in naturally synthesized proteins, or at least one modified or unusual amino acid, including but not limited to those shown on Table 1 below.

**TABLE 1**
**Modified and Unusual Amino Acids**

| Abbr. | Amino Acid | Abbr. | Amino Acid |
|---|---|---|---|
| Aad | 2-Aminoadipic acid | EtAsn | N-Ethylasparagine |
| Baad | 3- Aminoadipic acid | Hyl | Hydroxylysine |
| Bala | β-alanine, β-Amino-propionic acid | AHyl | allo-Hydroxylysine |
| Abu | 2-Aminobutyric acid | 3Hyp | 3-Hydroxyproline |
| 4Abu | 4- Aminobutyric acid, piperidinic acid | 4Hyp | 4-Hydroxyproline |
| Acp | 6-Aminocaproic acid | Ide | Isodesmosine |
| Ahe | 2-Aminoheptanoic acid | Alle | allo-Isoleucine |
| Aib | 2-Aminoisobutyric acid | MeGly | N-Methylglycine, sarcosine |
| Baib | 3-Aminoisobutyric acid | MeIle | N-Methylisoleucine |
| Apm | 2-Aminopimelic acid | MeLys | 6-N-Methyllysine |
| Dbu | 2,4-Diaminobutyric acid | MeVal | N-Methylvaline |
| Des | Desmosine | Nva | Norvaline |
| Dpm | 2,2'-Diaminopimelic acid | Nle | Norleucine |
| Dpr | 2,3-Diaminopropionic acid | Orn | Ornithine |
| EtGly | N-Ethylglycine | | |

In certain embodiments the proteinaceous composition comprises at least one protein, polypeptide or peptide. In further embodiments the proteinaceous composition comprises a biocompatible protein, polypeptide or peptide. As used herein, the term "biocompatible" refers to a substance which produces no significant untoward effects when applied to, or administered to, a given organism according to the methods and amounts described herein. Such untoward or undesirable effects are those such as significant toxicity or adverse immunological reactions. In preferred embodiments, biocompatible protein, polypeptide or peptide containing compositions will generally be viral proteins or peptides or synthetic proteins or peptides each essentially free from toxins, pathogens and harmful immunogens.

Proteinaceous compositions may be made by any technique known to those of skill in the art, including the expression of proteins, polypeptides or peptides through standard molecular biological techniques, the isolation of proteinaceous compounds from natural sources, or the chemical synthesis of proteinaceous materials. The nucleotide and protein, polypeptide and

peptide sequences for various genes have been previously disclosed, and may be found at computerized databases known to those of ordinary skill in the art. One such database is the National Center for Biotechnology Information's Genbank and GenPept databases (www.ncbi.nlm.nih.gov). The coding regions for these known genes may be amplified and/or expressed using the techniques disclosed herein or as would be know to those of ordinary skill in the art. Alternatively, various commercial preparations of proteins, polypeptides and peptides are known to those of skill in the art.

In certain embodiments a proteinaceous compound may be purified. Generally, "purified" will refer to a specific protein, polypeptide, or peptide composition that has been subjected to fractionation to remove various other proteins, polypeptides, or peptides, and which composition substantially retains its activity, as may be assessed, for example, by the protein assays, as would be known to one of ordinary skill in the art for the specific or desired protein, polypeptide or peptide. In still further embodiments, a proteinaceous compound may be purified to allow it to retain its native or non-denatured conformation. Such compounds may be recombinantly derived or they may be purified from endogenous sources.

In certain embodiments, the proteinaceous composition may comprise at least one antigen of a flaviviral envelope protein domain III that is recognized by an antibody. As used herein, the term "antibody" is intended to refer broadly to any immunologic binding agent such as IgG, IgM, IgA, IgD and IgE. Generally, IgG and/or IgM are preferred because they are the most common antibodies in the physiological situation and because they are most easily made in a laboratory setting.

The term "antibody" is also used to refer to any antibody-like molecule that has an antigen binding region, and includes antibody fragments such as Fab', Fab, $F(ab')_2$, single domain antibodies (DABs), Fv, scFv (single chain Fv), and the like. The techniques for preparing and using various antibody-based constructs and fragments are well known in the art. Means for preparing and characterizing antibodies are also well known in the art (See, *e.g.*, Harlow *et al.*, 1988; incorporated herein by reference).

It is contemplated that virtually any protein, polypeptide or peptide containing component may be used in the compositions and methods disclosed herein. However, it is preferred that the proteinaceous material is biocompatible. In certain embodiments, it is envisioned that the formation of a more viscous composition will be advantageous in that it will allow the composition to be more precisely or easily applied to the tissue and to be maintained in contact with the tissue throughout the procedure. In such cases, the use of a peptide composition, or more preferably, a polypeptide or protein composition, is contemplated. Ranges

of viscosity include, but are not limited to, about 40 to about 100 poise. In certain aspects, a viscosity of about 80 to about 100 poise is preferred.

*1. Variants of Flavivirus Envelope Protein Domain III Antigens*

Amino acid sequence variants of the polypeptides of the present invention can be substitutional, insertional or deletion variants. Deletion variants lack one or more residues of the native protein that are not essential for function or immunogenic activity, and are exemplified by the variants lacking a transmembrane sequence described above. Another common type of deletion variant is one lacking secretory signal sequences or signal sequences directing a protein to bind to a particular part of a cell. Insertional mutants typically involve the addition of material at a non-terminal point in the polypeptide. This may include the insertion of an immunoreactive epitope or simply a single residue. Terminal additions, called fusion proteins, are discussed below.

Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, such as stability against proteolytic cleavage, without the loss of other functions or properties. Substitutions of this kind preferably are conservative, that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine or histidine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine.

The term "functionally equivalent codon" is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine, and also refers to codons that encode biologically equivalent amino acids (see Table 2, below).

It also will be understood that amino acid and nucleic acid sequences may include additional residues, such as additional N- or C-terminal amino acids or 5' or 3' sequences, and yet still be essentially as set forth in one of the sequences disclosed herein, so long as the sequence meets the criteria set forth above, including the maintenance of immunogenicity or antibody binding. The addition of terminal sequences particularly applies to nucleic acid sequences that may, for example, include various non-coding sequences flanking either of the 5' or 3' portions

of the coding region or may include various internal sequences, *i.e.*, introns, which are known to occur within genes.

**TABLE 2**

**Codon Table**

| Amino Acids | | | Codons |
|---|---|---|---|
| Alanine | Ala | A | GCA GCC GCG GCU |
| Cysteine | Cys | C | UGC UGU |
| Aspartic acid | Asp | D | GAC GAU |
| Glutamic acid | Glu | E | GAA GAG |
| Phenylalanine | Phe | F | UUC UUU |
| Glycine | Gly | G | GGA GGC GGG GGU |
| Histidine | His | H | CAC CAU |
| Isoleucine | Ile | I | AUA AUC AUU |
| Lysine | Lys | K | AAA AAG |
| Leucine | Leu | L | UUA UUG CUA CUC CUG CUU |
| Methionine | Met | M | AUG |
| Asparagine | Asn | N | AAC AAU |
| Proline | Pro | P | CCA CCC CCG CCU |
| Glutamine | Gln | Q | CAA CAG |
| Arginine | Arg | R | AGA AGG CGA CGC CGG CGU |
| Serine | Ser | S | AGC AGU UCA UCC UCG UCU |
| Threonine | Thr | T | ACA ACC ACG ACU |
| Valine | Val | V | GUA GUC GUG GUU |
| Tryptophan | Trp | W | UGG |
| Tyrosine | Tyr | Y | UAC UAU |

The following is a discussion based upon changing of the amino acids of a protein to create an equivalent, or even an improved, second-generation molecule. For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid substitutions can be made in a protein sequence, and in its underlying DNA coding sequence, and nevertheless produce a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the DNA sequences of genes without appreciable loss of their biological utility or activity, as discussed below. Table 2, above, shows the codons that encode particular amino acids.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982). It is accepted that the

relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

It also is understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein. As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine *-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4).

It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still produce a biologically equivalent and/or an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those that are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions generally are based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, and size. Exemplary substitutions that take into consideration the various foregoing characteristics are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

Another embodiment for the preparation of polypeptides according to the invention is the use of peptide mimetics. Mimetics are peptide-containing molecules that mimic elements of protein secondary structure. See *e.g.*, Johnson (1993). The underlying rationale behind the use of peptide mimetics is that the peptide backbone of proteins exists chiefly to orient amino acid side chains in such a way as to facilitate molecular interactions, such as those of antibody and antigen. A peptide mimetic is expected to permit molecular interactions similar to the natural molecule. These principles may be used, in conjunction with the principles outlined above, to engineer second generation molecules having many of the properties of flavivirus envelope protein domain III antigens, but with altered and even improved characteristics.

*2. Fusion Proteins*

A specialized kind of insertional variant is the fusion protein. This molecule generally has all or a substantial portion of the native molecule, linked at the N- or C-terminus, to all or a portion of a second polypeptide. For example, fusions typically employ leader sequences from other species to permit the recombinant expression of a protein in a heterologous host. Another useful fusion includes the addition of a region to facilitate purification of the fusion protein. Inclusion of a cleavage site at or near the fusion junction will facilitate removal of the extraneous polypeptide after purification. Other useful fusions include linking of functional domains, such as active sites from enzymes such as a hydrolase, glycosylation domains, cellular targeting signals or transmembrane regions.

*3. Protein Purification*

It is desirable to purify flavivirus envelope protein domain III antigens or variants thereof. These techniques involve, at one level, the crude fractionation of the cellular milieu to polypeptide and non-polypeptide fractions. Certain embodiments of the invention are directed at preserving the conformation of flavivirus envelope protein domain III antigens as much as possible so that they are substantially non-denatured.

Antigens of the invention may be purified using gentle, non-denaturing detergents, which include, but are not limited to, NP40 and digitonin. Infected or transfected host cells may be solubilized using a gentle detergent. The following conditions are considered "substantially denaturing" or "denaturing": 10 mM CHAPS, 0.5% SDS, >2% deoxycholate, or 2.0% octylglucoside. Antigens prepared under such conditions would not be considered "non-denatured antigens." Preparations of substantially non-denatured antigens of the invention may be accomplished using techniques described in U.S. Patents 6,074,646 and 5,587,285, which are hereby incorporated by reference herein.

Certain aspects of the present invention concern the purification, and in particular embodiments, the substantial purification, of an encoded protein or peptide. The term "purified protein" or "purified peptide" as used herein, is intended to refer to a composition, isolatable from other components, wherein the protein or peptide is purified to any degree relative to its naturally-obtainable state. A purified protein or peptide therefore also refers to a protein or peptide, free from the environment in which it may naturally occur.

Generally, "purified" will refer to a protein or peptide composition that has been subjected to fractionation to remove various other components, and which composition substantially retains its expressed biological activity. Where the term "substantially purified" is used, this designation will refer to a composition in which the protein or peptide forms the major

component of the composition, such as constituting about 50%, about 60%, about 70%, about 80%, about 90%, about 95% or more of the proteins in the composition.

Various methods for quantifying the degree of purification of the protein or peptide will be known to those of skill in the art in light of the present disclosure. These include, for example, determining the specific activity of an active fraction, or assessing the amount of polypeptides within a fraction by SDS/PAGE analysis. A preferred method for assessing the purity of a fraction is to calculate the specific activity of the fraction, to compare it to the specific activity of the initial extract, and to thus calculate the degree of purity, herein assessed by a "-fold purification number." The actual units used to represent the amount of activity will, of course, be dependent upon the particular assay technique chosen to follow the purification and whether or not the expressed protein or peptide exhibits a detectable activity.

There is no general requirement that the protein or peptide always be provided in their most purified state. Indeed, it is contemplated that less substantially purified products will have utility in certain embodiments. Partial purification may be accomplished by using fewer purification steps in combination, or by utilizing different forms of the same general purification scheme. Methods exhibiting a lower degree of relative purification may have advantages in total recovery of protein product, or in maintaining the activity of an expressed protein.

*4. Antibodies*

The present invention concerns the detection of flavivirus, TBE serocomplex virus or West Nile virus antibodies using flavivirus, TBE virus or West Nile virus antigens. As used herein, the term "antibody" is intended to refer broadly to any immunologic binding agent such as IgG, IgM, IgA, IgD and IgE. Generally, IgG and/or IgM are preferred because they are the most common antibodies in the physiological situation and because they are most easily made in a laboratory setting. As described earlier, an antigen may include one or more epitopes and an antigen refers to any part of a polypeptide that contains at least one epitope.

The term "antibody" is used to refer to any antibody-like molecule that has an antigen binding region. The techniques for preparing and using various antibody-based constructs and fragments are well known in the art. Means for preparing and characterizing antibodies are also well known in the art (*See, e.g.*, Harlow and Lane, 1988; incorporated herein by reference).

In addition to polypeptides, antigens of the invention may be peptides corresponding to one or more antigenic determinants of the flavivirus envelope protein domain III polypeptides of the present invention. Thus, it is contemplated that detection of a flavivirus, a TBE virus or West Nile virus antibody may be accomplished with a flavivirus envelope protein domain III antigen that is a peptide or polypeptide.

Such peptides should generally be at least five or six amino acid residues in length and will preferably be about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25 or about 30 amino acid residues in length, and may contain up to about 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 111 or more residues and values there between. For example, these peptides may comprise a WN DIII antigen sequence, such as 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 110 or more contiguous amino acids from any of SEQ ID NO:3 or 11; or a TBE-DIII antigen, such as 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 110 or more contiguous amino acids from any of SEQ ID NO:14-20. Synthetic peptides will generally be about 35 residues long, which is the approximate upper length limit of automated peptide synthesis machines, such as those available from Applied Biosystems (Foster City, CA). Longer peptides also may be prepared, *e.g.*, by recombinant means.

U.S. Patent 4,554,101, incorporated herein by reference, teaches the identification and preparation of epitopes from primary amino acid sequences on the basis of hydrophilicity. Through the methods disclosed, one of skill in the art would be able to identify epitopes and/or antigens from within an amino acid sequence such as a flavivirus, TBE virus or West Nile virus sequence disclosed herein in as SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21.

Numerous scientific publications have also been devoted to the prediction of secondary structure, and to the identification of epitopes, from analyses of amino acid sequences (Chou and Fasman, 1974a, b; 1978a, b; 1979). Any of these may be used, if desired, to supplement the teachings of Hopp in U.S. Patent 4,554,101.

Moreover, computer programs are currently available to assist with predicting antigenic portions and epitopic core regions of proteins. Examples include those programs based upon the Jameson-Wolf analysis (Jameson and Wolf, 1988; Wolf *et al.*, 1988), the program PepPlot® (Brutlag *et al.*, 1990; Weinberger *et al.*, 1985), and other new programs for protein tertiary structure prediction (Fetrow and Bryant, 1993). Another commercially available software program capable of carrying out such analyses is MacVector (IBI, New Haven, CT).

In further embodiments, major antigenic determinants of flavivirus, TBE or West Nile envelope protein domain III polypeptide may be identified by an empirical approach in which portions of the gene encoding a flavivirus, TBE or West Nile envelope protein(s) are expressed in a recombinant host, and the resulting proteins tested for their ability to elicit an immune response. Alternatively all or part of flavivirus envelope proteins from different subtypes or clades of different flaviviruses may be tested. A range of peptides lacking successively longer

fragments of the C-terminus of the protein can be assayed as long as the peptides are prepared to retain their structure as it would be in a native polypeptide. The immunoactivity of each of these peptides is determined to identify those fragments or domains of the polypeptide that are immunodominant. Further studies in which only a small number of amino acids are removed at each iteration then allows the location of the antigenic determinants of the polypeptide to be more precisely determined.

Once one or more such analyses are completed, polypeptides are prepared that contain at least the essential features of one or more antigenic determinants. The peptides are then employed in the generation of antisera against the polypeptide. Minigenes or gene fusions encoding these determinants also can be constructed and inserted into expression vectors by standard methods, for example, using PCR™ cloning methodology.

*5. Immunodetection Methods*

As discussed, in some embodiments, the present invention concerns immunodetection methods for binding, purifying, removing, quantifying and/or otherwise detecting flavivirus antibodies in a sample, particularly TBE virus or West Nile virus antibodies, using DIII antigens. The samples may be any biological fluid or tissue from a patient or subject or animal host. The sample may be placed on a non-reactive surface such as a plate, slide, tube, or other structure that facilitates in any way the screening of the sample for flavivirus antibodies. While samples may be individually screened, large numbers of samples may be screened, such as for detecting contamination in blood bank samples.

Immunodetection methods include enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA), immunoradiometric assay, fluoroimmunoassay, chemiluminescent assay, bioluminescent assay, and Western blot, though several others are well known to those of ordinary skill. The steps of various useful immunodetection methods have been described in the scientific literature, such as, *e.g.*, Doolittle *et al.*, 1999; Gulbis *et al.*, 1993; De Jager *et al.*, 1993; and Nakamura *et al.*, 1987, each incorporated herein by reference.

In general, the immunobinding methods include obtaining a sample suspected of containing a flavivirus, in particular a TBE virus or a West Nile virus antibody with a composition comprising a flavivirus, TBE virus or West Nile DIII antigen in accordance with the present invention under conditions effective to allow the formation of immunocomplexes.

These methods include methods for purifying an antibody from bodily fluids, tissue or organismal samples. In these instances, the antigen removes the antibody component from a sample. The antigen will preferably be linked to a solid support, such as in the form of a column matrix, and the sample suspected of containing the antibody will be applied to the immobilized

antigen. The unwanted components will be washed from the column, leaving the antibody immunocomplexed to the immobilized antigen to be eluted. Alternatively, sandwich versions of this assay may be employed.

The immunobinding methods also include methods for detecting and quantifying the amount of an antibody component in a sample and the detection and quantification of any immune complexes formed during the binding process. Here, one would obtain a sample suspected of containing an antibody and contact the sample with an antigen, and then detect and quantify the amount of immune complexes formed under the specific conditions.

In terms of antigen detection, the biological sample analyzed may be any sample that is suspected of containing an antibody, such as, for example, a tissue section or specimen, a homogenized tissue extract, a cell, an organelle, separated and/or purified forms of any of the above antibody-containing compositions, or even any biological fluid that comes into contact with the cell or tissue, including blood and/or serum..

Contacting the chosen biological sample with the antigen under effective conditions and for a period of time sufficient to allow the formation of immune complexes (primary immune complexes) is generally a matter of simply adding the antigen composition to the sample and incubating the mixture for a period of time long enough for any antibodies present to form immune complexes with, *i.e.*, to bind to, antigens. After this time, the sample-antibody composition, such as a tissue section, ELISA plate, dot blot or western blot, will generally be washed to remove any non-specifically bound antibody species, allowing only those antibodies specifically bound within the primary immune complexes to be detected.

In general, the detection of immunocomplex formation is well known in the art and may be achieved through the application of numerous approaches. These methods are generally based upon the detection of a label or marker, such as any of those radioactive, fluorescent, biological and enzymatic tags. U.S. Patents concerning the use of such labels include 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149 and 4,366,241, each incorporated herein by reference. Of course, one may find additional advantages through the use of a secondary binding ligand such as a second antibody and/or a biotin/avidin ligand binding arrangement, as is known in the art.

The antigen employed in the detection may itself be linked to a detectable label, wherein one would then simply detect this label, thereby allowing the amount of the primary immune complexes in the composition to be determined. Alternatively, the first antigen that becomes bound within the primary immune complexes may be detected by means of a second binding ligand that has binding affinity for the antigen. In these cases, the second binding ligand may be

linked to a detectable label. The second binding ligand is itself often an antibody, which may thus be termed a "secondary" antibody. The primary immune complexes are contacted with the labeled, secondary binding ligand, or antibody, under effective conditions and for a period of time sufficient to allow the formation of secondary immune complexes. The secondary immune complexes are then generally washed to remove any non-specifically bound labeled secondary antibodies or ligands, and the remaining label in the secondary immune complexes is then detected.

Further methods include the detection of primary immune complexes by a two step approach. A second binding ligand, such as an antibody, that has binding affinity for the antibody is used to form secondary immune complexes, as described above. After washing, the secondary immune complexes are contacted with a third binding ligand or antibody that has binding affinity for the second antibody, again under effective conditions and for a period of time sufficient to allow the formation of immune complexes (tertiary immune complexes). The third ligand or antibody is linked to a detectable label, allowing detection of the tertiary immune complexes thus formed. This system may provide for signal amplification if this is desired.

*a. ELISAs*

As detailed above, immunoassays, in their most simple and/or direct sense, are binding assays. Certain preferred immunoassays are the various types of enzyme linked immunosorbent assays (ELISAs) and/or radioimmunoassays (RIA) known in the art. Immunohistochemical detection using tissue sections is also particularly useful. However, it will be readily appreciated that detection is not limited to such techniques. Western blotting, dot blotting, FACS analyses, peptide arrays may also be used to detect antigen/antibody interaction.

Turning first to immunoassays, in their most simple and direct sense, preferred immunoassays of the invention include the various types of enzyme linked immunosorbent assays (ELISAs) known to the art. However, it will be readily appreciated that the utility of the DIII preparations described herein are not limited to such assays, and that other useful embodiments include RIAs and other non-enzyme linked antibody binding assays or procedures.

In some embodiments of the ELISA assay, flavivirus, TBE virus or West Nile virus envelope proteins or appropriate peptides incorporating DIII antigen sequences are immobilized onto a selected surface, preferably a surface exhibiting a protein affinity such as the wells of a polystyrene microtiter plate. After washing to remove incompletely adsorbed material, one will desire to bind or coat a nonspecific protein such as bovine serum albumin (BSA), casein, solutions of milk powder, gelatin, PVP, superblock, or horse albumin onto the well that is known to be antigenically neutral with regard to the test antisera. This allows for blocking of

nonspecific adsorption sites on the immobilizing surface and thus reduces the background caused by nonspecific binding of antisera onto the surface. Following an appropriate coating period (for example, 3 hours), the coated wells will be blocked with a suitable protein, such as bovine serum albumin (BSA), casein, solutions of milk powder, gelatin, PVP, superblock, or horse albumin, and rinsed several times (e.g., 4 or 5 times) with a suitable buffer, such as PBS. The wells of the plates may then be allowed to dry, or may instead be used while they are still wet.

After binding of antigenic material to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface is contacted with the antisera or clinical or biological extract to be tested in a manner conducive to immune complex (antigen/antibody) formation. Such conditions preferably include diluting the antisera with diluents such as BSA, bovine gamma globulin (BGG) and phosphate buffered saline (PBS)/Tween. These added agents also tend to assist in the reduction of nonspecific background. The layered antisera is then allowed to incubate for from 1 to 4 hours, at temperatures preferably on the order of 20° to 25°C. Following incubation, the antisera-contacted surface is washed so as to remove non-immunocomplexed material. A preferred washing procedure includes washing with a solution such as PBS/Tween, or borate buffer.

Following formation of specific immunocomplexes between the test sample and the bound antigen, and subsequent washing, the occurrence and even amount of immunocomplex formation may be determined by subjecting same to a second antibody having specificity for the first. Of course, in that the test sample will typically be of human origin, the second antibody will preferably be an antibody having specificity in general for human IgG, IgM or IgA. To provide a detecting means, the second antibody will preferably have an associated enzyme that will generate a color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one will desire to contact and incubate the antisera–bound surface with a urease, alkaline phosphatase, or peroxidase-conjugated anti-human IgG for a period of time and under conditions which favor the development of immunocomplex formation (*e.g.*, incubation for 2 hours at room temperature in a PBS-containing solution such as PBS–Tween).

After incubation with the second enzyme-tagged antibody, and subsequent to washing to remove unbound material, the amount of label is quantified by incubation with a chromogenic substrate such as urea and bromocresol purple or 2,2'-azino-di-(3-ethylbenzthiazoline-6-sulfonic acid (ABTS) and $H_2O_2$, in the case of peroxidase as the enzyme label. Quantification is then achieved by measuring the degree of color generation, *e.g.*, using a visible spectra spectrophotometer.

In an exemplary embodiment, in each of the microtiter wells will be placed about 10 µl of the test patient sample along with about 90 µl of reaction buffer (*e.g.*, PBS with about 1% digitonin or other mild protein solubilizing agent). Control wells of the ELISA plate will include normal sera (human sera without flavivirus antibody), and anti-flavivirus antibody collected from subjects.

Irrespective of the format employed, ELISAs have certain features in common, such as coating, incubating and binding, washing to remove non-specifically bound species, and detecting the bound immune complexes. These are described below.

In coating a plate with either antigen or antibody, one will generally incubate the wells of the plate with a solution of the antigen or antibody, either overnight or for a specified period of hours. The wells of the plate will then be washed to remove incompletely adsorbed material. Any remaining available surfaces of the wells are then "coated" with a nonspecific protein that is antigenically neutral with regard to the test antisera. These include bovine serum albumin (BSA), casein or solutions of milk powder. The coating allows for blocking of nonspecific adsorption sites on the immobilizing surface and thus reduces the background caused by nonspecific binding of antisera onto the surface.

In ELISAs, it is probably more customary to use a secondary or tertiary detection means rather than a direct procedure. Thus, after binding of a protein or antibody to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface is contacted with the biological sample to be tested under conditions effective to allow immune complex (antigen/antibody) formation. Detection of the immune complex then requires a labeled secondary binding ligand or antibody, and a secondary binding ligand or antibody in conjunction with a labeled tertiary antibody or a third binding ligand.

"Under conditions effective to allow immune complex (antigen/antibody) formation" means that the conditions preferably include diluting the antigens and/or antibodies with solutions such as BSA, bovine gamma globulin (BGG) or phosphate buffered saline (PBS)/Tween. These added agents also tend to assist in the reduction of nonspecific background.

The "suitable" conditions also mean that the incubation is at a temperature or for a period of time sufficient to allow effective binding. Incubation steps are typically from about 1 to 2 to 4 hours or so, at temperatures preferably on the order of 25°C to 27°C, or may be overnight at about 4°C or so.

Following all incubation steps in an ELISA, the contacted surface is washed so as to remove non-complexed material. An example of a washing procedure includes washing with a

solution such as PBS/Tween, or borate buffer. Following the formation of specific immune complexes between the test sample and the originally bound material, and subsequent washing, the occurrence of even minute amounts of immune complexes may be determined.

To provide a detecting means, the second or third antibody will have an associated label to allow detection. This may be an enzyme that will generate color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one will desire to contact or incubate the first and second immune complex with a urease, glucose oxidase, alkaline phosphatase or hydrogen peroxidase-conjugated antibody for a period of time and under conditions that favor the development of further immune complex formation (*e.g.*, incubation for 2 hours at room temperature in a PBS-containing solution such as PBS-Tween).

After incubation with the labeled antibody, and subsequent to washing to remove unbound material, the amount of label is quantified, *e.g.*, by incubation with a chromogenic substrate such as urea, or bromocresol purple, or 2,2'-azino-di-(3-ethyl-benzthiazoline-6-sulfonic acid (ABTS), or $H_2O_2$, in the case of peroxidase as the enzyme label. Quantification is then achieved by measuring the degree of color generated, *e.g.*, using a visible spectra spectrophotometer.

*b. Assay Plates*

In some embodiments, the wells of the assay plates may first be coated with an anti-DIII, antiTBE-DIII and/or anti-WN-DIII antibody. This would immobilize DIII antigen to the plastic in the presence of a mild solubilizing buffer, such as from about 0.1% to about 10% digitonin (particularly about 1% digitonin). Such an approach is particularly efficacious in preparing assay plates with wells made of plastic.

The assay plates in other embodiments of the invention comprise a multiplicity of microtiter wells, and in some embodiments, polystyrene microtiter wells. These wells would be coated with about 500 ng/well of the rDIII, TBE-rDIII or WN-rDIII antigen.

*c. Immunohistochemistry*

The antigens of the present invention may also be used in conjunction with both fresh-frozen and/or paraffin-embedded tissue blocks prepared for study by immunohistochemistry (IHC). Flavivirus, TBE virus and West Nile virus antibodies may be identified in this manner. The method of preparing tissue blocks from these particulate specimens has been successfully used in previous IHC studies of various prognostic factors, and/or is well known to those of skill in the art (Brown *et al.*, 1990; Abbondanzo *et al.*, 1990; Allred *et al.*, 1990).

## III. NUCLEIC ACID MOLECULES

In some embodiments, the present invention concerns envelope protein domain III antigens prepared from genomic or recombinant nucleic acids. Some of the teachings herein pertain to the construction, manipulation, and use of nucleic acids to produce a recombinant envelope protein domain III antigen.

### A. Polynucleotides Encoding E protein domain III Envelope Antigens

The present invention concerns polynucleotides, isolatable from cells or viruses, that are free from cellular or viral genomic DNA or RNA and are capable of expressing all or part of a protein or polypeptide. The polynucleotide may encode a peptide or polypeptide containing all or part of an envelope protein domain III amino acid sequence or may encode a peptide or polypeptide having an envelope protein domain III antigen sequence. Recombinant proteins can be purified from expressing cells to yield denatured or non-denatured proteins or peptides.

As used herein, the term "DNA segment" refers to a DNA molecule that has been isolated free of total genomic DNA of a particular species or genomic RNA of a virus. Therefore, a DNA segment encoding a polypeptide refers to a DNA segment that contains wild-type, polymorphic, or mutant polypeptide-coding sequences yet is isolated away from, or purified free from, total viral RNA or, mammalian, or human genomic DNA. Included within the term "DNA segment" are recombinant vectors, including, for example, plasmids, cosmids, phage, viruses, and the like.

As used in this application, the term "envelope protein domain III (DIII) polynucleotide" refers to an envelope protein domain III polypeptide-encoding nucleic acid molecule that has been isolated free of total genomic nucleic acid. Therefore, a "polynucleotide encoding an envelope protein domain III antigen" refers to a DNA segment that contains all or part of envelope protein domain III polypeptide-coding sequences isolated away from, or purified free from, total viral genomic nucleic acid.

It also is contemplated that a particular polypeptide from a given species or strain may be represented by natural variants that have slightly different nucleic acid sequences but, nonetheless, encode the same protein (see above).

Similarly, a polynucleotide comprising an isolated or purified gene refers to a DNA segment including, in certain aspects, regulatory sequences, isolated substantially away from other naturally occurring genes or protein encoding sequences. In this respect, the term "gene" is used for simplicity to refer to a functional protein, polypeptide, or peptide-encoding unit. As will be understood by those in the art, this functional term includes genomic sequences, cDNA

sequences, RNA sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, domains, peptides, fusion proteins, and mutants. A nucleic acid encoding all or part of a native or modified polypeptide may contain a contiguous nucleic acid sequence encoding all or a portion of such a polypeptide of the following lengths: about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 441, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, 1000, 1010, 1020, 1030, 1040, 1050, 1060, 1070, 1080, 1090, 1095, 1100, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 9000, 10000, or more nucleotides, nucleosides, or base pairs, which may be contiguous nucleotides encoding any length of contiguous amino acids of SEQ ID NO:2, or any of SEQ ID NO:3-21.

In particular embodiments, the invention concerns isolated DNA segments and recombinant vectors incorporating DNA sequences that encode a DIII antigen polypeptide or peptide, such as all or part of DIII, which includes within its amino acid sequence a contiguous amino acid sequence in accordance with, or essentially corresponding to a native polypeptide. Thus, an isolated DNA segment or vector containing a DNA segment may encode, for example, a DIII antigen that is capable of binding to an anti-flavivirus antibody. The term "recombinant" may be used in conjunction with a polypeptide or the name of a specific polypeptide, and this generally refers to a polypeptide produced from a nucleic acid molecule that has been manipulated *in vitro* or that is the replicated product of such a molecule.

Encompassed by certain embodiments of the present invention are DNA segments encoding relatively small peptides, such as, for example, a peptide comprising all or part of an envelope protein DIII antigen (including at least one epitope) of any subtype or clade of flavivirus.

The nucleic acid segments used in the present invention, regardless of the length of the coding sequence itself, may be combined with other nucleic acid sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol.

It is contemplated that the nucleic acid constructs of the present invention may encode full-length envelope protein from any flaevivirus or encode a truncated version of the polypeptide, for example a truncated envelope protein domain III polypeptide, such that the transcript of the coding region represents the truncated version. The truncated transcript may then be translated into a truncated protein. Alternatively, a nucleic acid sequence may encode a full-length polypeptide sequence with additional heterologous coding sequences, for example to allow for purification of the polypeptide, transport, secretion, post-translational modification, or for therapeutic benefits such as targeting or efficacy. As discussed above, a tag or other heterologous polypeptide may be added to the modified polypeptide-encoding sequence, wherein "heterologous" refers to a polypeptide that is not the same as the modified polypeptide.

In a non-limiting example, one or more nucleic acid constructs may be prepared that include a contiguous stretch of nucleotides identical to or complementary to a particular gene, such as a envelope protein gene of a particular flavivirus or subtype or strain of a flavivirus. A nucleic acid construct may be at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1,000, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000 nucleotides in length, as well as constructs of greater size, up to and including chromosomal sizes (including all intermediate lengths and intermediate ranges), given the advent of nucleic acids constructs such as a yeast artificial chromosome are known to those of ordinary skill in the art. It will be readily understood that "intermediate lengths" and "intermediate ranges," as used herein, means any length or range including or between the quoted values (*i.e.*, all integers including and between such values).

The DNA segments used in the present invention encompass immunologically or biologically functional equivalent modified polypeptides and peptides. Such sequences may arise as a consequence of codon redundancy and functional equivalency that are known to occur naturally within nucleic acid sequences and the proteins thus encoded. Alternatively, functionally equivalent proteins or peptides may be created via the application of recombinant DNA technology, in which changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being exchanged. Changes designed by human may be introduced through the application of site-directed mutagenesis techniques, *e.g.*, to introduce improvements to the antigenicity of the protein, to reduce toxicity effects of the protein *in vivo* to a subject given the protein, or to increase the efficacy of any treatment involving the protein.

The sequence of a flavivirus envelope protien DIII polypeptide will substantially correspond to a contiguous portion of that shown in amino acids 292-402 of SEQ ID NO:3 or

any of SEQ ID NO:4-21 and have relatively few amino acids that are not identical to, or an immunological or a biologically functional equivalent of, the amino acids shown in amino acids 292-402 of SEQ ID NO:3 or any of SEQ ID NO:4-21. The term "immunologically functional equivalent" or "biologically functional equivalent" is well understood in the art and is further defined in detail herein to include an ability to bind or be recognized by a specific flavivirus antibody.

Accordingly, sequences that have between about 70% and about 80%; or more preferably, between about 81% and about 90%; or even more preferably, between about 91% and about 99%; of amino acids that are identical or functionally equivalent to the amino acids of SEQ ID NO:3-21 will be sequences that are "essentially as set forth in SEQ ID NO:3-21."

In certain other embodiments, the invention concerns isolated DNA segments and recombinant vectors that include within their sequence a contiguous nucleic acid sequence from that shown in SEQ ID NO:1. This definition is used in the same sense as described above and means that the nucleic acid sequence substantially corresponds to a contiguous portion of that shown in SEQ ID NO:1 and has relatively few codons that are not identical, or functionally equivalent, to the codons of SEQ ID NO:1. The term "functionally equivalent codon" is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine, and also refers to codons that encode biologically equivalent amino acids. See Table 2 above, which lists the codons preferred for use in humans, with the codons listed in decreasing order of preference from left to right in the table (Wada *et al.*, 1990). Codon preferences for other organisms also are well known to those of skill in the art (Wada *et al.*, 1990, included herein in its entirety by reference).

The various probes and primers designed around the nucleotide sequences of the present invention may be of any length. By assigning numeric values to a sequence, for example, the first residue is 1, the second residue is 2, *etc.*, an algorithm defining all primers can be proposed:

$$n \text{ to } n + y$$

where n is an integer from 1 to the last number of the sequence and y is the length of the primer minus one, where n + y does not exceed the last number of the sequence. Thus, for a 10-mer, the probes correspond to bases 1 to 10, 2 to 11, 3 to 12 ... and so on. For a 15-mer, the probes correspond to bases 1 to 15, 2 to 16, 3 to 17 ... and so on. For a 20-mer, the probes correspond to bases 1 to 20, 2 to 21, 3 to 22 ... and so on.

It also will be understood that this invention is not limited to the particular nucleic acid encoding amino acid sequences of SEQ ID NO:2, or any of SEQ ID NO:3-21. Recombinant

vectors and isolated DNA segments may therefore variously include the envelope protein DIII antigen-coding regions themselves, coding regions bearing selected alterations or modifications in the basic coding region, or they may encode larger polypeptides that nevertheless include envelope protein DIII antigen-coding regions or may encode biologically functional equivalent proteins or peptides that have variant amino acids sequences.

*1. Vectors*

Native and modified polypeptides may be encoded by a nucleic acid molecule comprised in a vector. The term "vector" is used to refer to a carrier nucleic acid molecule into which a nucleic acid sequence can be inserted for introduction into a cell where it can be replicated. A nucleic acid sequence can be "exogenous," which means that it is foreign to the cell into which the vector is being introduced or that the sequence is homologous to a sequence in the cell but in a position within the host cell nucleic acid in which the sequence is ordinarily not found. Vectors include plasmids, cosmids, viruses (bacteriophage, animal viruses, and plant viruses), and artificial chromosomes (*e.g.*, YACs). One of skill in the art would be well equipped to construct a vector through standard recombinant techniques, which are described in Sambrook *et al.*, (2001) and Ausubel *et al.*, 1996, both incorporated herein by reference. In addition to encoding a modified polypeptide such as modified envelope protein DIII, a vector may encode non-modified polypeptide sequences such as a tag or targeting molecule. Useful vectors encoding such fusion proteins include pIN vectors (Inouye *et al.*, 1985), vectors encoding a stretch of histidines, and pGEX or pMAL vectors, for use in generating glutathione S-transferase (GST) or maltose binding protein (MBP) soluble fusion proteins for later purification and separation or cleavage. A targeting molecule is one that directs the modified polypeptide to a particular organ, tissue, cell, or other location in a subject's body.

The term "expression vector" refers to a vector containing a nucleic acid sequence coding for at least part of a gene product capable of being transcribed. In some cases, RNA molecules are then translated into a protein, polypeptide, or peptide. Expression vectors can contain a variety of "control sequences," which refer to nucleic acid sequences necessary for the transcription and possibly translation of an operably linked coding sequence in a particular host organism. In addition to control sequences that govern transcription and translation, vectors and expression vectors may contain nucleic acid sequences that serve other functions as well and are described *infra*.

Vectors may include a "promoter," which is a control sequence that is a region of a nucleic acid sequence at which initiation and rate of transcription are controlled. It may contain genetic elements at which regulatory proteins and molecules may bind such as RNA polymerase

and other transcription factors. The phrases "operatively positioned," "operatively linked," "under control," and "under transcriptional control" mean that a promoter is in a correct functional location and/or orientation in relation to a nucleic acid sequence to control transcriptional initiation and/or expression of that sequence. A promoter may or may not be used in conjunction with an "enhancer," which refers to a cis-acting regulatory sequence involved in the transcriptional activation of a nucleic acid sequence.

A specific initiation signal also may be required for efficient translation of coding sequences. These signals include the ATG initiation codon or adjacent sequences. Exogenous translational control signals, including the ATG initiation codon, may need to be provided. One of ordinary skill in the art would readily be capable of determining this and providing the necessary signals. It is well known that the initiation codon must be "in-frame" with the reading frame of the desired coding sequence to ensure translation of the entire insert. The exogenous translational control signals and initiation codons can be either natural or synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements.

In certain embodiments of the invention, the use of internal ribosome entry sites (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements are able to bypass the ribosome scanning model of 5'— methylated Cap dependent translation and begin translation at internal sites (Pelletier and Sonenberg, 1988). IRES elements from two members of the picornavirus family (polio and encephalomyocarditis) have been described (Pelletier and Sonenberg, 1988), as well an IRES from a mammalian message (Macejak and Sarnow, 1991). IRES elements can be linked to heterologous open reading frames. Multiple open reading frames can be transcribed together, each separated by an IRES, creating polycistronic messages. By virtue of the IRES element, each open reading frame is accessible to ribosomes for efficient translation. Multiple genes can be efficiently expressed using a single promoter/enhancer to transcribe a single message (see U.S. Patent 5,925,565 and 5,935,819, herein incorporated by reference).

The vectors or constructs of the present invention will generally comprise at least one termination signal. A "termination signal" or "terminator" is comprised of the DNA sequences involved in specific termination of an RNA transcript by an RNA polymerase. Thus, in certain embodiments a termination signal that ends the production of an RNA transcript is contemplated. A terminator may be necessary *in vivo* to achieve desirable message levels.

In eukaryotic systems, the terminator region may also comprise specific DNA sequences that permit site-specific cleavage of the new transcript so as to expose a polyadenylation site.

This signals a specialized endogenous polymerase to add a stretch of about 200 A residues (polyA) to the 3′ end of the transcript. RNA molecules modified with this polyA tail appear to more stable and are translated more efficiently. Thus, in other embodiments involving eukaryotes, it is preferred that that terminator comprises a signal for the cleavage of the RNA, and it is more preferred that the terminator signal promotes polyadenylation of the message. The terminator and/or polyadenylation site elements can serve to enhance message levels and/or to minimize read through from the cassette into other sequences.

Terminators contemplated for use in the invention include any known terminator of transcription described herein or known to one of ordinary skill in the art, including but not limited to, for example, the termination sequences of genes, such as for example the bovine growth hormone terminator or viral termination sequences, such as for example the SV40 terminator. In certain embodiments, the termination signal may be a lack of transcribable or translatable sequence, such as due to a sequence truncation.

In expression, particularly eukaryotic expression, one will typically include a polyadenylation signal to effect proper polyadenylation of the transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and/or any such sequence may be employed. Preferred embodiments include the SV40 polyadenylation signal and/or the bovine growth hormone polyadenylation signal, convenient and/or known to function well in various target cells. Polyadenylation may increase the stability of the transcript or may facilitate cytoplasmic transport.

In order to propagate a vector in a host cell, it may contain one or more origins of replication sites (often termed "ori"), which is a specific nucleic acid sequence at which replication is initiated. Alternatively an autonomously replicating sequence (ARS) can be employed if the host cell is yeast.

*2. Host Cells*

As used herein, the terms "cell," "cell line," and "cell culture" may be used interchangeably. All of these terms also include their progeny, which is any and all subsequent generations. It is understood that all progeny may not be identical due to deliberate or inadvertent mutations. In the context of expressing a heterologous nucleic acid sequence, "host cell" refers to a prokaryotic or eukaryotic cell, and it includes any transformable organism that is capable of replicating a vector and/or expressing a heterologous gene encoded by a vector. A host cell can, and has been, used as a recipient for vectors. A host cell may be "transfected" or "transformed," which refers to a process by which exogenous nucleic acid, such as a modified

protein-encoding sequence, is transferred or introduced into the host cell. A transformed cell includes the primary subject cell and its progeny.

Host cells may be derived from prokaryotes or eukaryotes, including yeast cells, insect cells, and mammalian cells, depending upon whether the desired result is replication of the vector or expression of part or all of the vector-encoded nucleic acid sequences. Numerous cell lines and cultures are available for use as a host cell, and they can be obtained through the American Type Culture Collection (ATCC), which is an organization that serves as an archive for living cultures and genetic materials (www.atcc.org). An appropriate host can be determined by one of skill in the art based on the vector backbone and the desired result. A plasmid or cosmid, for example, can be introduced into a prokaryote host cell for replication of many vectors. Bacterial cells used as host cells for vector replication and/or expression include DH5α, JM109, and KC8, as well as a number of commercially available bacterial hosts such as SURE® Competent Cells and SOLOPACK™ Gold Cells (STRATAGENE®, La Jolla, CA). Alternatively, bacterial cells such as *E. coli* LE392 could be used as host cells for phage viruses. Appropriate yeast cells include *Saccharomyces cerevisiae*, *Saccharomyces pombe*, and *Pichia pastoris*.

Examples of eukaryotic host cells for replication and/or expression of a vector include Vero, HeLa, NIH3T3, Jurkat, 293, COS, CHO, Saos, and PC12. Many host cells from various cell types and organisms are available and would be known to one of skill in the art. Similarly, a viral vector may be used in conjunction with either a eukaryotic or prokaryotic host cell, particularly one that is permissive for replication or expression of the vector.

Some vectors may employ control sequences that allow it to be replicated and/or expressed in both prokaryotic and eukaryotic cells. One of skill in the art would further understand the conditions under which to incubate all of the above described host cells to maintain them and to permit replication of a vector. Also understood and known are techniques and conditions that would allow large-scale production of vectors, as well as production of the nucleic acids encoded by vectors and their cognate polypeptides, proteins, or peptides.

*3. Expression Systems*

Numerous expression systems exist that comprise at least a part or all of the compositions discussed above. Prokaryote- and/or eukaryote-based systems can be employed for use with the present invention to produce nucleic acid sequences, or their cognate polypeptides, proteins and peptides. Many such systems are commercially and widely available.

The insect cell/baculovirus system can produce a high level of protein expression of a heterologous nucleic acid segment, such as described in U.S. Patent No. 5,871,986, 4,879,236, both herein incorporated by reference, and which can be bought, for example, under the name

MAXBAC® 2.0 from INVITROGEN® and BACPACK™ BACULOVIRUS EXPRESSION SYSTEM FROM CLONTECH®.

In addition to the disclosed expression systems of the invention, other examples of expression systems include STRATAGENE®'s COMPLETE CONTROL™ Inducible Mammalian Expression System, which involves a synthetic ecdysone-inducible receptor, or its pET Expression System, an *E. coli* expression system. Another example of an inducible expression system is available from INVITROGEN®, which carries the T-REX™ (tetracycline–regulated expression) System, an inducible mammalian expression system that uses the full-length CMV promoter. INVITROGEN® also provides a yeast expression system called the *Pichia methanolica* Expression System, which is designed for high-level production of recombinant proteins in the methylotrophic yeast *Pichia methanolica*. One of skill in the art would know how to express a vector, such as an expression construct, to produce a nucleic acid sequence or its cognate polypeptide, protein, or peptide.

## IV. KITS AND DIAGNOSTICS

The exemplary studies described herein show that rDIII is an excellent tool for differentiating infections caused by TBE serogroup versus mosquito-borne flaviviruses. This reagent would be particularly useful in regions where tick-borne and/or mosquito-borne flaviviruses are endemic, such as Asia, Europe and North America as well as economically depressed countries as it is relatively simple and inexpensive to produce.

The studies described herein extend and improve upon the use of recombinant flavivirus envelope protein DIII for the detection of TBE and/or WN virus infection. Recombinant DIII derived from the WN virus was found to be very specific and highly sensitive for identifying infection in naturally infected primates. Embodiments of the invention use rDIII as a diagnostic reagent for detecting TBE serocomplex virus infections. Assays using rDIII specific homologous and heterologous antiserum demonstrated a very high degree of sensitivity and specificity and tests using mouse hyperimmune serum supported these results. A potential drawback of the rDIII-based diagnostic assay may be the inability to differentiate between the TBE serocomplex viruses. It is contemplated that the minimization of potential binding epitopes may be accomplished by using peptide based diagnostic assays. Peptide based assays may be used to produce a greater degree of specificity to differentiate the TBE serocomplex of viruses immunologically. In other embodiments of the invention, the use of the rDIII-based ELISAs as a rapid preliminary test for TBE virus infection can be followed by further clinical and laboratory tests such as virus isolation or neutralization assays to conclusively identify the virus causing

disease. In certain embodiments, rDIII can be used in a "dipstick" format by cross-linking the C-terminus of the protein to a solid substrate. This format would allow complete exposure of all rDIII antibody epitopes to test sera. The rDIII is an extremely stable protein as was shown by retention of the structure of TBE rDIII in up to 4M urea, 2M guanidinium hydrochloride and at low pH. The physical properties of the rDIII would lend themselves to the use of the rDIII reagent in unfavorable environmental conditions such as extreme heat or cold, or after extended storage. Recombinant protein technology for making these diagnostics reagents will also minimize the cost of diagnosis, which in turn will make the use of such reagents feasible in economically depressed countries.

In yet another aspect of the invention, a kit is envisioned for anti-flavivirus, anti-TBE virus or anti-West Nile virus antibody detection. In some embodiments, the present invention contemplates a diagnostic kit for detecting anti-TBE or anti-West Nile virus antibodies and human TBE or West Nile virus infection. The kit comprises reagents capable of detecting the anti-TBE or anti-West Nile antibody immunoreactive with the native or recombinant DIII antigens described here. Reagents of the kit include at least one DIII antigen, such as all or part of a TBE DIII and/or West Nile DIII, and any of the following: another DIII antigen, buffers, secondary antibodies or antigens, or detection reagents, or a combination thereof.

In some embodiments, the kit may also comprise a suitable container means, which is a container that will not react with components of the kit, such as an eppendorf tube, an assay plate, a syringe, or a tube. In specific embodiments, the kit comprises an array or chip on which one or more DIII antigen(s) is placed or fixed, such as those described in Reneke *et al.*, 1998, which is herein incorporated by reference.

In other embodiments of the invention, in addition to comprising a DIII antigen, it comprises a secondary antibody capable of detecting the anti-flavivirus, anti-TBE virus or anti-West Nile virus antibody that is immunoreactive with the recombinant DIII antigen.

The flavivirus antigen reagent of the kit can be provided as a liquid solution, attached to a solid support or as a dried powder. Preferably, when the reagent is provided in a liquid solution, the liquid solution is an aqueous solution. Preferably, when the reagent provided is attached to a solid support, the solid support can be chromatograph media, peptide array plate, plastic beads or plates, or a microscope slide. When the reagent provided is a dry powder, the powder can be reconstituted by the addition of a suitable solvent. In yet other embodiments, the kit may further comprise a container means comprising an appropriate solvent.

In some embodiments, the kit comprises a container means that includes a volume of a second antibody, such as goat anti-human IgG or IgM conjugated with alkaline phosphatase or

other anti-human Ig secondary antibody, and a second container means that includes a volume of a buffer comprising a non-denaturing solubilizing agent, such as about 1% digitonin.

The kit may in other embodiments further comprise a third container means that includes an appropriate substrate, such as PNPP for alkaline phosphatase, or 9-dianisidine for peroxidase. A fourth container means that includes an appropriate "stop" buffer, such as 0.5 m NaOH, may also be included with various embodiments of the kit.

The kit may further include an instruction sheet that outlines the procedural steps of the assay, and will follow substantially the same steps as the typical EIA format known to those of skill in the art.

## EXAMPLES

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

### EXAMPLE 1

### Materials and Methods

Virus strains and antigens

Strains of WN, JE, and St. Louis encephalitis (SLE) viruses used in this study are listed in Table 3. All viruses were obtained from the World Arbovirus Reference Collection at the University of Texas Medical Branch at Galveston (UTMB). The WN strains were chosen to represent subtypes of both genetic lineages I and II; genotypes of these viruses had previously been determined by sequencing of a region corresponding to the NS5/3'-non-coding region junction. The protocols for propagation and nucleotide sequencing of these viruses have been described elsewhere (Beasley *et al.*, 2002).

Whole virus suckling mouse brain-derived antigen preparations for WN (strain 385-99), JE (strain Nakayama), SLE (strain Parsons) and MVE viruses were also obtained from the World Arbovirus Reference Collection.

**TABLE 3.** Origins and genotypes of West Nile virus strains.

| Strain | Origin | Year of Isolation | Lineage* | Designation |
|---|---|---|---|---|
| 385-99 | United States | 1999 | I | USA99b |
| EthAn4766 | Ethiopia | 1976 | I | ETH76 |
| TL443 | Israel | 1952 | I | ISR52 |
| Goldblum | Israel | 1953 | I | ISR53 |
| MRM16 | Australia | 1960 | I (Kunjin) | AUS60 |
| 804994 | India | 1980 | I (Indian) | IND80 |
| DakAnMg798 | Madagascar | 1978 | II | MAD78 |
| SPU116-89 | South Africa | 1989 | II | SA89 |
| DakArMg-979 | Madagascar | 1988 | II | MAD88 |
| H-442 | South Africa | 1958 | II | SA58 |

Recombinant WN strain 385-99 envelope protein domain III

A fragment corresponding to structural domain III of the WN virus strain 385-99 envelope protein (amino acids 296-415) was RT-PCR amplified for cloning and expression as a glutathione S-transferase (GST) fusion using the pGEX-2T system (Amersham Pharmacia Biotech, Piscataway NJ). Protocols for expression and purification of the WN recombinant structural domain III of the envelope protein GST fusion protein (rDIII GST), followed by cleavage of the fusion protein and purification of WN rDIII away from the GST fusion partner, were based on those described by Bhardwaj *et al.* (2001). Briefly, RNA was extracted from culture supernatant of virus-infected Vero cells using the QiaAmp kit (Qiagen Inc., Valencia CA) and reverse transcribed using the AMV Reverse Transcriptase with random hexamer primers (Roche). Specific fragments representing envelope protein structural domain III with 5′ and 3′ restriction sites suitable for cloning were amplified using Taq polymerase (Roche). PCR products were gel purified, cloned into pGEM-TEasy (Promega Corp., Madison WI), digested using the appropriate restriction enzymes and subcloned into appropriately digested pGEX-2T vector. Inserts were sequenced in both directions to ensure fidelity of the products. Recombinant expression plasmids were transformed into DH5α *E. coli* for propagation and protein expression. Following induction, the fusion protein was purified on a glutathione sepharose column, and rDIII was subsequently cleaved from GST using thrombin (Novagen,

Madison WI) and purified on a DEAE anion exchange column. Homogeneity of rDIII was confirmed by mass spectroscopy (data not shown).

Antisera and monoclonal antibodies

WN rDIII expressed and purified using the GST system was sent to Harlan Bioproducts for Science (Indianapolis, IN) to be used as an antigen for the preparation of a polyclonal rabbit serum. The antiserum was prepared using Harlan's standard immunization protocol in New Zealand White Rabbits (details available at "www.hbps.com"). Three WN Envelope protein reactive MAbs (5H10, 5C5 and 7H2) were obtained from Bioreliance Cop. (Rockville MD). The binding of these MAbs to domain III, differences in their specificities, and the identification of putative binding sites for 5C5 and 5H10 are described elsewhere (Beasley and Barrett, 2002). Additional polyclonal mouse hyper-immune ascitic fluids (HIAF) against WN, JE, SLE, MVE, dengue type 2 (DEN2) and yellow fever (YF) viruses were obtained from the World Arbovirus Reference Collection.

Plaque reduction neutralization tests (PRNT)

Ten-fold dilutions of virus ($10^{-1}$ to $10^{-6}$) were prepared in MEM tissue culture medium (Sigma) containing 2% fetal bovine serum (FBS) and mixed with equal volumes of anti-WN MAb or polyclonal anti-WN-rDIII serum, diluted 1/200 or 1/20 respectively, or MEM media only. Virus-antibody mixtures were incubated at room temperature for 60 minutes before inoculation into monolayers of Vero cells in 6-well tissue culture plates (Corning Inc., Corning NY). Plates were incubated at room temperature for 30 minutes to allow virus adsorption, then overlayed with 5 mL per well of MEM medium containing 1% agarose (MEM/agarose). After incubation at 37°C/5% $CO_2$ for a suitable period (two or three days for WN virus strains; four or five days for JE/SLE viruses) wells were overlayed with an additional 2 mL of MEM/agarose containing 2% v/v neutral red solution (Sigma, St. Louis MO). Plaques were counted the following day and neutralization indices determined as the $\log_{10}$ reduction in virus titer in the presence of MAb/polyclonal serum compared with the medium only control.

Indirect ELISA assays

The wells of 96-well microtiter plates (Corning Inc.) were coated overnight at 4°C with either WN, JE, MVE, or SLE virus antigen (equivalent to one pH 6.2 HA unit), or WN-rDIII protein (25 ng/well), diluted in borate saline (pH 9.0). These optimal dilutions of whole virus and recombinant antigens had been determined previously by titration against specific antisera

(data not shown). Wells were blocked for 60 minutes with a solution of 3% bovine serum albumin in phosphate buffered saline (PBS) containing 5% tween-20 (PBS/tween), and then washed with PBS/tween. Serial doubling dilutions (1:100 - 1:6400) of anti-WN, -JE, -SLE, -MVE, -DEN2 and -YF mouse HIAFs were prepared in duplicate columns, the plates were incubated at room temperature for 45 minutes, and then washed four times with PBS/tween. Peroxidase-labeled anti-mouse immunoglobulin serum (Sigma) diluted 1:2500 in PBS/tween was added to each well, and plates were again incubated, washed (four times with PBS/tween, twice with PBS) and antibody binding visualized by addition of TMB substrate (Sigma). After incubating for 10 minutes at room temperature, color reactions were stopped by addition of 3M HCl and absorbances read at 490 nm on a Fluoromark plate reader (BioRad, Hercules CA).

Nucleotide sequencing

RNA was extracted from WN virus-infected Vero cell supernatants and reverse transcribed as described earlier. A fragment that included the structural domain III coding sequence was RT-PCR amplified using primers WN1751 (5'-$_{1751}$TGCATCAAGCTTTGGCTGGA$_{1770}$)(SEQ ID NO:22) and WN2504A (5'-$_{2504}$TCTTGCCGGCTGATGTCTAT$_{2485}$)(SEQ ID NO:23) for lineage I strains, or WN1739 (5'-$_{1751}$TGCACCAAGCTCTGGCCGGA$_{1770}$)(SEQ ID NO:24) and WN2498A (5'-$_{2510}$CGGAGCTCTTGCCTGCCAAT$_{2491}$)(SEQ ID NO:25) for lineage II strains. Primer pairs were designed based on Genbank sequences AF196835 and M12294 (each of which is incorporated herein by reference), respectively, and are numbered according to residues in the AF196835 sequence. PCR products of the appropriate sizes were gel purified and directly sequenced using the ABI PRISM Big Dye v3.0 cycle sequencing kit (Applied Biosystems) on an ABI PRISM 3100 genetic analyzer (Applied Biosystems) according to the manufacturer's protocols. Sequence analysis was performed using the Vector NTI Suite package (Informax Inc.).

**Results**

Specificity of Polyvalent Anti-WN Domain III Serum

To determine the specificity of polyvalent anti–domain III rabbit serum PRNT assays and Western blot with related JE serocomplex and other mosquito-borne flaviviruses were performed. In PRNT assays, the anti-domain III serum neutralized WN strain 385-99 by more than 5000-fold (Table 4), while less than 10-fold reductions in titre were observed in assays with JE, SLE, DEN or YF viruses. In Western blot assays with JE, MVE and SLE virus antigen

preparations the inventors observed some weak cross-reactivity with the envelope proteins of those viruses (FIG. 3). In other western blot analysis the WN domain III specific monoclonal antibodies were characterized (FIG. 4).

TABLE 4. Variable neutralization of West Nile virus strains representative of genetic lineages I and II by Envelope protein domain III-specific monoclonal antibodies and a polyclonal antiserum

| NEUTRALIZATION INDEX* AGAINST WN VIRUS STRAINS | | | | |
|---|---|---|---|---|
| | Serum | | | |
| WN strain | 5H10 | 7H2 | 5C5 | Anti-DIII |
| USA99b | 2.3 | 3.6 | 2.5 | 3.8 |
| ETH76 | 2.7 | 4.2 | 2.4 | 3.9 |
| ISR52 | 2.2 | 3.4 | 2.4 | 3.9 |
| ISR53 | 0.9 | 2.1 | 1.9 | 3.9 |
| AUS60 | 1.1 | 1.6 | 1.1 | 2.0 |
| IND80 | 1.7 | 2.6 | 2.5 | ≥ 5.6 |
| MAD78 | 2.5 | 3.1 | 2.5 | ≥ 4.8 |
| SA89 | 1.3 | 1.7 | 1.2 | 2.7 |
| MAD88 | 0.2 | 0.1 | -0.2 | 0.3 |
| SA58 | 0.2 | 0.1 | 0.1 | 0.6 |

*neutralization index is $\log_{10}$ reduction in virus titre in the presence of Mab/polyclonal serum compared with culture medium only control

Variable Neutralization of WN Virus Strains by Anti-Domain III Serum and MAbs

Having observed the specificity of the anti-domain III serum for WN virus in PRNT assays (FIG. 5), the inventors then tested whether this reagent could distinguish between subtypes of WN virus. In addition, the subtype specificity of the neutralizing domain III reactive MAbs was examined. Although differences in neutralization did not clearly delineate viruses of different genetic lineages, some variable neutralization of WN subtypes was observed (Table 4). In general, viruses of genetic lineage I were efficiently neutralized by both the polyclonal serum and the MAbs (~500- to 5000-fold reductions in titre), although neutralization of strain AUS60 (lineage I, Kunjin) was approximately 10 to 100-fold lower than that of other lineage I strains. Similarly, strain ISR53 was less efficiently neutralized by the MAbs than other lineage I strains,

although this strain was still strongly neutralized by the polyclonal anti-domain III serum. Lineage II virus strain MAD78 was also strongly neutralized by MAbs and polyclonal serum, while strains MAD88 and SA58 completely escaped neutralization (less than 10-fold reductions in titer in the presence of either MAbs or serum). Neutralization of strain SA89 was incomplete (10- to 100-fold reductions in titer only) and was comparable to that of AUS60.

Correlation of Domain III Amino Acid Sequence with Neutralization Phenotype

Analysis of derived Envelope protein domain III amino acid sequences for each WN strain studied allowed the identification of residues that appeared to influence their neutralization phenotype (FIG. 6). Strains USA99b and ETH76 were identical throughout the region examined, while other lineage I strains differed at only one (ISR52 and ISR53) or three (AUS60, IND80) residues. Strain ISR53, which partially escaped neutralization by the MAbs but not the polyclonal serum (Table 4), contained a Thr→Ala substitution at E332 (amino acid 332 of the enevelope protein). Strain AUS60, which partially escaped neutralization by MAbs and antiserum, differed at residues E310 (Lys→Thr), E339 (Val→Ile) and E366 (Ala→Ser) although the substitution at E339 was also observed in strain IND80, which did not escape neutralization. Additional substitutions in IND80 were identified at E312(Leu→Val) and E390(Glu→Asp). A His→Tyr substitution at E398 of strain ISR52 did not affect the neutralization of this strain. The lineage II strains studied all differed from USA99b at between two and four residues in domain III (FIG. 6). Strain SA89, which displayed partial escape from neutralization by MAbs and antiserum, contained the smallest number of substitutions, with changes at E312 (Leu→Ala) and E369 (Ala→Ser). Strains MAD88 and SA58, which escaped neutralization by MAbs and anti-domain III serum, shared the substitutions at E312 and E369, and contained an additional substitution at E332 (Thr→Lys). Strain MAD78, which was efficiently neutralized by both MAbs and antiserum, contained the greatest number of variable amino acids. This strain contained the E369 (Ala→Ser) substitution observed in the other lineage II strains examined, a Leu→Val change at E312 (also present in IND80), and additional unique substitutions at E371 (Val→Ile) and E375 (Leu→Ile).

Comparison with representative amino acid sequences of the comparable region of JE, SLE and MVE viruses revealed much greater variation, and substitutions were present at each of the critical residues for neutralization that were identified in the WN virus strains, and also at clusters of residues around these loci (FIG. 6).

Enhanced Specificity of WN r-DIII in Indirect Elisa Compared with Whole Virus Antigens

The apparent type-specificity of functional epitopes in domain III (as evidenced by the limited neutralizing activity of the anti-domain III serum against other JE serocomplex viruses and some strains of WN lineage II) led us to investigate the utility of rDIII as an antigen for serological assays. Indirect ELISAs were performed using a panel of MIAF raised against several mosquito-borne flaviviruses (see Materials and Methods).

In assays where plates were coated with whole virus antigens (inactivated WN, JE, MVE or SLE viruses) extensive cross-reactivity was observed with most MIAF antisera (FIG. 7). In general, the strongest reactions were observed between specific antigen/antiserum combinations (*e.g.* anti-WN serum with WN antigen). However, in each case, as least two other antisera reacted to at least 75% of the homologous serum at dilutions between 1 :100 and 1:800. The binding activity of the anti-MVE MIAF was lower than the other JE serocomplex antisera in each assay, however its cross-reactive binding to WN, JE or SLE antigens was at least 60% of its binding to the MVE antigen.

In contrast, the binding of anti-WN MIAF to WN rDIII antigen cleaved from a MBP fusion was clearly discriminated from the other antisera; values at dilutions between 1 :200 and 1 :6400 were at least three-fold higher than those of sera raised against other flavivirus antigens (FIG. 7). The peak values obtained using the rDIII antigen were approximately 75% of those with whole virus WN antigen indicating some loss of sensitivity, as would be expected with the removal of binding sites contained in the remainder of the envelope protein.

Further studies have shown that WN rDIII antigen cleaved from a GST fusion protein yields greater specificity in indirect ELISA assays compared with whole virus antigen preparations (FIG. 8). Ninety-six-well ELISA plates were coated with sucrose-acetone extracted virus antigens (WN, JE, SLE or MVE equivalent to 4 HA units at pH6.2) or WN rDIII antigen. Serial dilutions of polyclonal mouse antisera raised against WN, JE, SLE, MVE, DEN or YF viruses were added to wells of plates (optimal antigen and antiserum dilutions had been determined by block titration of homologous antigen(Ag)/antibody(Ab) pairs); 2° Ab was HRP anti-mouse Ig; substrate was TMB.

Additional studies showed that the use of cleaved, purified WN rDIII antigen yields greater specificity in indirect ELISA assays than use of purified MBP-DIII fusion protein antigen (FIG. 9). In brief, 96–well ELISA plates were coated with either (a) WN rDIII Ag (~15 ng/well) or WN rDIII as an MBP fusion (~35 ng/well and ~1.75 ng/well total protein in (b) and (c)

respectively, which represents ~7 ng/well or 0.35 ng/well WN rDIII). Assays were performed using serial dilutions of polyclonal mouse sera as described previously. Note greater cross-reactive (possibly non-specific) binding in panel (b). Further dilution of MBP rDIII fusion protein antigen reduces apparent cross reactivity but with marked reduction in sensitivity.

**EXAMPLE 2**

**Materials and Methods**

Generation of recombinant Domain III:

Recombinant domain III (rDIII) protein was expressed in *E. coli* as a fusion protein using maltose-binding protein (MBP) as the fusion partner. Expression and purification was essentially following the manufacturer's instructions and was previously described. Briefly, the coding sequence for domain III of the viral envelope protein was cloned into the pMAL-c2x expression vector (New England Biolabs). The individual DIII molecules encompassed approximately residues 300-395 of the viral envelope protein. Cloning into the pMAL system added an additional serine to the N-terminus of the recombinant proteins. The fusion protein was expressed by induction with IPTG. Purification was achieved *via* lysing the cells by sonication followed by affinity purification over an amylose resin column (New England Biolabs). The fusion protein was cleaved with Factor Xa (Novagen) and the MBP and rDIII separated by size exclusion chromatography on a Superdex 75 column (Amersham/Pharmacia). Domain III was concentrated and stored at 4°C until use. The TBE rDIII protein has been found to extremely stable under very stringent conditions (Bhardwaj *et al.* 2001, White *et al.*, 2003) and is stable when stored at 4°C for extended periods.

Antiserum production:

Purified rDIII was provided to Harlan Bioproducts for Science (Indianapolis, IN) for production of rabbit antisera. Antiserum against each rDIII protein was produced in two New Zealand white rabbits. Testing of the antisera in ELISA and western blot assays found little difference between antisera generated in different rabbits against the same antigen (M. Holbrook, unpublished observations).

Antigens and mouse immune ascitic fluids:

Suckling mouse brain-derived viral antigens from dengue-2 (DEN2), dengue-4 (DEN4), yellow fever (YF) vaccine strain 17D, Japanese encephalitis (JE) strain Nakayama, Langat (LGT) strain TP21 and Powassan (POW) strain LB were obtained from the World Arbovirus Reference Collection housed at the University of Texas Medical Branch. In addition, mouse

hyperimmune ascitic fluid (MIAF) against DEN2, DEN4, JE, YF, West Nile (WN), LGT, POW, KFD and RSSE were also obtained from the World Arbovirus Reference Collection.

Western blots:

Ten nanograms (ng) of purified rDIII was run on 12% SDS-PAGE gels and transferred to a nitrocellulose membrane for blotting. The blots were blocked with TBS-tween (20 mM Tris, pH 7.5, 150 mM NaCl, 0.05% tween 20) containing 3% dry milk powder (Blotto) for at least 30 min. at room temperature. The membranes were probed for 1 hr at room temperature with the appropriate antiserum diluted in Blotto at dilutions of 1:800-1:1000 dependent upon the antiserum. Blots were washed 3 times with Blotto and probed with a goat anti-rabbit-horseradish peroxidase (HRP) conjugated secondary antibody (Sigma) at a 1:2000 dilution in Blotto for 1 hr at room temperature. The blots were subsequently washed twice with Blotto and three times with TBS-tween. The presence of rDIII was detected using the ECL chemiluminescence substrate (Amersham/Pharmacia).

Indirect ELISAs:

Purified rDIII or mouse brain-derived viral antigen (Ag) was coated onto 96-well round bottom microtiter plates (Falcon) overnight at 4°C in borate saline buffer (120 mM NaCl, 50 mM boric acid, pH 9.0). Preliminary experiments examining sensitivity of the assay found that wells coated with 10-20 ng of rDIII provided optimum sensitivity while Ag was coated in plates at 1 hemagglutination (HA) unit per well. Wells were blocked with PBS-tween (PBS with 0.5% tween-20) containing 3% bovine serum albumin (BSA) for 30 min. at room temperature then washed once with PBS-tween prior to incubation with antisera. Two-fold serial dilutions of antisera were made in duplicate wells. All dilutions were made in PBS-tween. Following a 1 hr room temperature incubation with primary antibody, the plates were washed with PBS-tween and then incubated with either goat anti-mouse or goat anti-rabbit HRP conjugated secondary antibody at a 1:2000 dilution for 1 hr at room temperature. The plates were washed and then incubated with 50 µl 3,3',5,5'-Tetramethylbenzidine (TMB) (Sigma) colorometric detection reagent for 5 min at room temperature. The reaction was stopped with 50 µl 3M HCl and the plates were read at 450 nm with a reference wavelength of 595 nm.

**Results**

Cloning of viral DIII:

The rDIII used in these assays were cloned from viruses representing several mosquito-borne flaviviruses and the major clades of the TBE serocomplex with the exception of the Siberian and Far-eastern subtypes of viruses (FIG. 10). Viral RNA for the Siberian and Far-eastern subtypes was not available as they are BSL-4 agents with restricted availability. Kumlinge (KUM) virus is a strain of CEE while OHF and KFD viruses are viruses that cause hemorrhagic fever rather than an exclusively encephalitic disease and form distinct subgroups within the serocomplex. LGT and POW viruses also represent distinct subgroups of the TBE serocomplex (FIG. 10). LGT is a naturally attenuated virus originally isolated in Malaysia and POW may represent an older lineage of TBE viruses in North America and Asia (Gould *et al.*, 2001, Zanotto *et al.*, 1995). In addition to members of the TBE serocomplex, rDIII from the mosquito-borne WN, YF vaccine strain 17D and YF wild-type strain Asibi were also produced. The amino acid sequence within the DIII of all flaviviruses is similar, but the level of identity within the TBE serocomplex is quite high (FIG. 16). This high degree of similarity makes these viruses difficult to distinguish serologically.

Western blots:

Purified rDIII derived from several mosquito- and tick-borne flaviviruses were run on SDS-PAGE gels and transferred to nitrocellulose for blotting with homologous and heterologous rabbit anti-rDIII specific antiserum. These assays found a significant degree of cross-reactivity between rDIII derived from members of the tick-borne flavivirus serocomplex (FIG. 11). All five TBE serocomplex antisera recognized the five TBE serocomplex rDIII, though the sera tended to cross-react less well with LGT rDIII, and the rabbit anti-POW rDIII antiserum appeared to have less cross-reactivity than other sera. This result is not surprising as LGT and POW viruses are phylogenetically less related than KUM, OHF and KFD viruses (FIG. 10). None of the rabbit anti-TBE serocomplex antisera recognized rDIII derived from the mosquito-borne flaviviruses WN or YF, nor did rabbit anti-YF or anti-WN antisera recognize any of the TBE rDIII (FIG. 11).

Viral antigen based ELISAs:

Mouse brain-derived viral antigens were coated in 96-well plates at one hemagglutination (HA) unit per well. DIII specific sera and MIAF were diluted at two-fold serial dilutions and sensitivity and specificity of the assay determined. As seen in FIG. 12 there is a lack of

specificity for TBE serogroup viral antigens using MIAF. MIAF generated against tick-borne flaviviruses are shown in open symbols while the remaining symbols comprise mosquito-borne flaviviruses. In all assays JE MIAF cross-reacted strongly with all of the antigens tested. The assay that demonstrated clear specificity was that against JE mouse-derived antigen where the JE MIAF clearly reacted well with the antigen. In the remaining panels, little specificity was found for MIAF binding to mouse-brain derived viral antigen clearly demonstrating that this antigen is not suitable for a diagnostic assay. In these experiments, the MIAF were not normalized against homologous rDIII or virus-derived antigens prior to performing the studies. Instead, the MIAF were tested as received from the World Arbovirus Reference Collection. Due to the lack of availability of sera from natural infections, this method was undertaken to mimic the testing of a potentially infected individual in a true diagnostic setting. In some cases, such as is apparent with JE virus MIAF, the reactive antibody titer may be higher than other MIAF and give a higher level of cross-reactivity. Normalization of the MIAF might reduce the cross-reactivity, but it would also bias the study.

In similar studies using rabbit anti-rDIII specific antiserum to screen against virus-derived antigen, cross-reactivity was also observed. As seen in FIG. 13, though the degree of cross-reactivity is not as great as was seen in FIG. 12, both rabbit rDIII antiserum specific for the DIII of LGT and WN viruses reacted with several viral antigens. Even though specific antiserum was used in the assay, based on results from western blots (FIG. 11), significant cross reactivity between mosquito-borne virus antigens and antisera specific for tick-borne viruses was found. Again, the antisera were not normalized prior to use in these studies. These results, in conjunction with those shown in FIG. 11, demonstrate that the use of mouse brain-derived viral antigen in a diagnostic assay does not provide the specificity required to conclusively identify to agent responsible during flavivirus infection.

The majority of the mouse brain-derived viral antigens tested in these experiments were representative of the mosquito-borne flaviviruses. Unfortunately, the assay could not be performed using more TBE serocomplex antigens as some were not available from the World Arbovirus Reference Collection and others that were available in the collection could not be tested due to concerns about the complete inactivation of the virus during antigen preparation (*i.e.*, live virus might be in the antigen preparations) and inadequate facilities for tested potentially infectious antigens (*e.g.*, BSL-4 for OHF and KFD antigens).

Domain III based ELISAs

ELISAs using rDIII as the antigen, rather than mouse brain-derived viral antigen, demonstrated a much more specific reaction against homologous rDIII-specific antiserum. Both WN and YF rDIII reacted only with homologous serum (true for both YF wild-type Asibi strain and vaccine 17D strain rDIII) (FIG. 14F-14H). The YF-Asibi rDIII rabbit antiserum cross-reacted with rDIII derived from YF vaccine strain 17D, an expected result as these envelope proteins are nearly identical (FIG. 14G). A similar result was seen in YF-17D rDIII coated plates (FIG. 14H). Recombinant DIII derived from the TBE serocomplex of viruses, however, were not specific for individual virus rDIII specific rabbit antisera, but were cross-reactive with rDIII derived from viruses only within the TBE serocomplex (FIG. 14A-14E, open symbols represent tick-borne flaviviruses). This result supports the western blot data presented in FIG. 11 where cross-reactivity was seen between the rabbit antisera generated against the recombinant proteins of the TBE serocomplex. These assays found that TBE serocomplex derived rDIII cross-reacted with all of the TBE serocomplex specific rabbit anti-rDIII antisera, but not those derived from the mosquito-borne WN or YF viruses. This assay was also quite sensitive as serum diluted to 1:320 could easily be detected above a 0.2 OD450 cut-off for a positive test. The cross-reactivity among the TBE serocomplex viruses was somewhat expected as the level of amino acid identity among the envelope protein DIII from these viruses is very high (FIG.16).

To examine the ability of rDIII to detect the presence of IgG in a model for analysis of test serum from a potentially infected individual, MIAF were assayed in plates coated with rDIII in experiments similar to those shown above using mouse brain-derived viral antigen. In these experiments, it was found that the rDIII coated plates were able to clearly differentiate MIAF derived from TBE serocomplex infected animals from those of mosquito-borne viruses (FIG. 15). As seen in panels A-E of FIG. 15, TBE serocomplex rDIII cross-reacted with the majority of the TBE serocomplex MIAF tested. As with previous figures, TBE serocomplex specific MIAF are shown in open symbols. POW MIAF seemed to cross-react with all of the TBE rDIII whereas the RSSE MIAF was somewhat less reactive. POW MIAF was also the only MIAF to react with OHF rDIII and with considerably less sensitivity than the other rDIII coated plates (FIG. 15E). Unfortunately, OHF specific MIAF was not available from the World Arbovirus Reference Collection. Recombinant DIII for mosquito-borne flaviviruses was also highly specific as the WN MIAF reacted only with WN rDIII, as was previously shown (FIG. 15F) and the YF-17D rD3 reacted with YF MIAF (FIG. 15G) though the sensitivity of this assay was not as high as with the TBE serocomplex rDIII or WN rDIII. Both of the YF rDIII cross-reacted with JE MIAF indicating potentially similar surface amino acid residues.

## REFERENCES

The following references, to the extent that they provide exemplary procedural or other details supplementary to those set forth herein, are specifically incorporated herein by reference.

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